

FIG. 1A

MAJORITY	ATGXXGGCGATGCTTCCCCCTCTTTGAGCCCAAGGCCGGGTCTCTCTGGTGACGGGCACCACTGGCCT	
DNAPTAQ	...AG..G.....G.....G.....	70
DNAPTFL	.....C..G.....	67
DNAPTTH	...GA.....G.....A.....	70
MAJORITY	ACCGCACCTTCTTCGCCCTGAAGGGCCTCACCACCACCGGGGGAACCGGTGCAGGGGTCTACGGCTT	
DNAPTAQ	.....CA.....G..G.....	140
DNAPTFL	.....T.....C.....C..T.....	137
DNAPTTH	.....G.....	140
MAJORITY	CGCCAAGAGCCTCCTCAAGGCCCTGAAGGAGGACGGGGACXXGCCGGTGTCTTGTGACGCCAAG	
DNAPTAQ	.....C.....A.....	207
DNAPTFL	...A.....GT..T.....	204
DNAPTTH	.....T..AA..C..CT.....	280
MAJORITY	GCCCCCTCCTTCGCGCCACGAGGCCTACGAGGCCTACAAGCGGGCGGGCCCCACCCCGGAGGACTTTC	
DNAPTAQ	.....G..GG.....G.....	277
DNAPTFL	.....GA.....G.....C.....	274
DNAPTTH	.....G.....C.....	280
MAJORITY	CCCGGCAGCTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCTTGGCGGCCTCGAGGTCCCCGGCTA	
DNAPTAQ	.....A.....G.....G.....	347
DNAPTFL	.....G.....T.....A..C.....T..G..G.....T.....	344
DNAPTTH	.....T.....T..A..C.....	350

FIG. 2A

MAJORITY	CGAGGCGGACGACGT	CTGGCCACCCCTGGCC	AAGGCGGAAAGGAGGGGTACGAGGTGCGCATCCTC	
DNAPTAQ	.....C.....G.....	.....C.....	.....C.....	417
DNAPTFL	T.....G.....CG.....	.....	.....	414
DNAPTTH	.....T..C.....	.....	.....	420
MAJORITY	ACCGCCGACCGGACCTCTAC	CAGCTCCTTTCCGACCGCATCGCCGTCTCCACCCCGAGGGGTACCTCA		
DNAPTAQ	.....AAA.....T.....	.....CA.....	.....	487
DNAPTFL	..T.....	.....G..G.....A.....T.....	.....G..	484
DNAPTTH	.....	.....A..G.C.....G.....	.....CC.....	490
MAJORITY	TCACCCCGCGGTGGCTTTGGGAGAGTACGGCCTGAGGCCGGAGCAGTGGGTGACTACCGGCCCTGGC			
DNAPTAQ	.....C.....A.....	.....C..C.....CC.....	.....A..	557
DNAPTFL	.....AC.....	.....C.C.....	.....	554
DNAPTTH	.....A.....	.....C.....	.....T..C.....C.T	560
MAJORITY	GGGGACCCCTCCGACAACTCTCCCGGGGTCAAGGGCATCGGGGAGAGACCGCCXGAAGCTCCTCXAG			
DNAPTAQ	C.....GAG.....	.....T.....	.....G..GAG.....T..GG..	627
DNAPTFL	.....G..T..A.....	.....G.....	.....A..G....A..CGC	624
DNAPTTH	.....	.....	.....TC.....A..	630
MAJORITY	GAGTGGGGAGCCTGGAAACCTCCTCAAGAACCTGGACCGGGTGAAGCCCGC	..CXTCCGGGAGAAGA		
DNAPTAQ	.....GC.....	.....C.....	.....A.....	694
DNAPTFL	.....	.....T..C..C.....	.....T..G.....C	691
DNAPTTH	.....A.....	.....A.....	.....A.AAA.G.....	700

FIG. 2B

MAJORITY	TCCAGGCCCCACATGGAXGACCTGAXGCTCTCCTGGGAGCTXTCCCAGGTGCGCACCGACCTGCCCCCTGGA	
DNAPTAQ	...T...C...T...A...C...GG...A...	764
DNAPTFL	...GGG...G...C...GCC...T...C...A...T...A...T...	761
DNAPTTH	...A...C...A...C...G...T...C...G...C...C...	770
MAJORITY	GGTGGACTTCGCCCAAGXGGCGGGAGCCCCGACCGGGAGGGGCTTAGGGCCCTTCTGGAGAGGCTGGAGTTT	
DNAPTAQ	...AA...AA...A...A...T...T...T...T...	834
DNAPTFL	...GG.G.C.C..CACA...A...T...T...GC...T...T...C..T...	831
DNAPTTH	...C...C...G...C...G...C...C...C...C...C...	840
MAJORITY	GGCAGCCTCCTCCACGAGTTCGGGCCTCCTGGAGGGCCCCCAAGGCCCTGGAGGAGGCCCCCTGGCCCCCGC	
DNAPTAQ	...T...AA...T...G...G...G...G...G...G...	904
DNAPTFL	...A...G...G...G...G...G...G...G...G...G...T...	901
DNAPTTH	...G...G...G...G...G...G...G...G...G...G...	910
MAJORITY	CGGAAGGGGCCTTCGTGGGCTTTGTCCCTTTCCCGCCCCGAGCCCCATGTGGGCCGAGCTTCTGGCCCTGGC	
DNAPTAQ	...G...G...G...G...G...G...G...G...G...G...	974
DNAPTFL	...T..TT...TC.T...T...T...T...T...T...T...	971
DNAPTTH	...C...C...C...C...C...C...C...C...C...C...AAA...	980
MAJORITY	CGCCGCCAGGGAGGGCCGGGTCCACCGGGCACCAGACCCCTTTAXGGGCCTXAGGGACCTXAAGGAGGTG	
DNAPTAQ	...G...G...G...G...G...G...G...G...G...G...C...C...C...C...	1044
DNAPTFL	T.GG..GT...G..CC...T...A...C...G...G...G...G...G...T...G...G...	1041
DNAPTTH	...TG...C...G...G...G...G...G...G...G...G...G...G...A..A...C...C...C...C...	1050

FIG. 2C

MAJORITY	CGGGGXCTCCTCGCCCAAGGACCTGGCCGTTTTTGGCCCTGAGGGAGGGCCTXGACCTCXTGCCCCGGGGACG	
DNAPTAQ	.....G..T.....A.....AG.....C.....A.....T.G.....CC.....C.....	1114
DNAPTFL	.....AA.....G.....G.....C.....C.....T.C..A.A.....	1111
DNAPTTH	.....C.....C.....C.....TC.....G..A.....G.....G.....	1120
MAJORITY	ACCCCATGCTCCTCGCCTACCTCCTGGACCCCTCCAACACCACCCCGAGGGGTGGCCCCGGCGCTACGG	
DNAPTAQ	.....T.....	1184
DNAPTFL	.....G.....T.....T.....T.....	1181
DNAPTTH	.....G.....G.....	1190
MAJORITY	GGGGGAGTGGACGGAGGAXGCGGGGAGCGGGCCCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXXGGAG	
DNAPTAQ	C.....G.....G.....GC.....T.....GCC.....GTG..G.	1254
DNAPTFL	.....T.....A.....GG.....C.C.....A..C...AAA.....	1260
DNAPTTH	.....C..C.CCC.C.....C..G.....CAT.G.....CCTTA..	1260
MAJORITY	CGCCTTGAGGGGAGGAGGGCTCCTTTGGCTTTACCAGGAGGTGGAGAAGCCCTTTCCCGGGTCCIGG	
DNAPTAQ	A.G.....G.....G.....G.....GCT.....	1324
DNAPTFL	.....A...A..A..AC.C..G.....G.....G.....GT...	1321
DNAPTTH	.....C.....A.....C.....C.....A.....C.....	1330
MAJORITY	CCCACATGGAGGCCACGGGGGTXCGGCTGGACGTGGCCTACCTCCAGGCCCTXTCCCTGGAGGTGGCGGA	
DNAPTAQ	.....G..C.....T...AG.....T.G.....C...	1394
DNAPTFL	..GG.....C.....C.....C.....A..C	1391
DNAPTTH	.....C.....A.....T.....T.....C.T.....	1400

FIG.2D

MAJORITY	GGAGATCCGCCCTCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCCGGGAC	
DNAPTAQ	.....GC.....CC.....	1464
DNAPTFL	.....G.G.....AG..G.....C.....	1461
DNAPTTH	.....T.....T.....G.....	1470
MAJORITY	CAGCTGGAAGGGTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAAGACXGGCAAGC	
DNAPTAQ	.....C.....A.....C.....	1534
DNAPTFL	.....GC.....G.C..G..T.....G..G..A..	1531
DNAPTTH	.....TA.....T.G..G.....C.A.....A.....	1540
MAJORITY	GCTCCACCAGCGCCCGTGCTGGAGGCCCTXCGXGAGGCCACCCCATCTGTGGAGAAGATCCTGCAGTA	
DNAPTAQ	.....C.....C..C.....	1604
DNAPTFL	.....T.....G..A.....CCGC.....	1601
DNAPTTH	.....G.....A..G.....C...C..	1610
MAJORITY	CCGGGAGCTCACCAAGCTCAAGAACACCTACATXGACCCCTGCGCXGXCTCGTCCACCCAGGACGGGC	
DNAPTAQ	.....G...G.....T.....T...G.A...A.....	1674
DNAPTFL	.....A.....A.....C.C..G.....A..C...C...	1671
DNAPTTH	.....G.G.....AAG.....G.....	1680
MAJORITY	CGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTTAGTAGCTCCGACCCCAACCTGC	
DNAPTAQ	.....A.....A.....T.....C..	1744
DNAPTFL	.....G.....C.....TCC.....	1741
DNAPTTH	.....G.....G.....	1750

FIG. 2E

MAJORITY	AGAAATCCCCGTCGACACCCXCTGGGCCAGAGGATCCGCCGGGCTTCGTGGCCGAGGAGGGXTGGGT	
DNAPTAQ	.....G..T..G.....A.C.....G...C.	1814
DNAPTFL	.....G.....T.....C.C.....A.....C.....	1811
DNAPTTH	.....CT.....C.....T.....C	1820
MAJORITY	GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCCTGGCCACCTCTCCGGGGACGAGAACCTG	
DNAPTAQ	A.....A.....G.....C.....	1884
DNAPTFL	.C.....T.T.....C.....T.....	1881
DNAPTTH	.....C.....C.....A.....	1890
MAJORITY	ATCCGGGTCTTCCAGGAGGGAGGACATCCACCCAGACCCGACGCTGGATGTTCCGGCGTCCCCCCGG	
DNAPTAQ	.....C.....GG.....G..	1954
DNAPTFL	.....T.....A.....TT.....C.	1951
DNAPTTH	...A.....A.....A.....	1960
MAJORITY	AGGCCGTGGACCCCTGATGCGCCGGCGGCCAAGACCATCAACTTCGGGGTCCTCTACGGCATGTCGGC	
DNAPTAQ	.....G..	2024
DNAPTFL	.A.GG..A.....T.....G.....	2021
DNAPTTH	.....GG.G.....C.....	2030
MAJORITY	CCACCGCCTCTCCCAGGAGCTTGCCCATCCCCCTACGAGGAGGGGTGGCCCTTCATTGAGCGCTACTTCCAG	
DNAPTAQ	.....A.....T.....CCA.....T...	2094
DNAPTFL	.....GG.....T.....	2091
DNAPTTH	...TA.G.....T..A.....A	2100

FIG. 2F

MAJORITY	AGCTTCCCCAAGGTGCGGGCCTGGATTGAGAAAGACCCTGGAGGAGGCGAGGCGGGGTACGTGGAGA	
DNAPTAQ	.....	2164
DNAPTFL	...A.....GG.....C.....C.CC.....T.....	2161
DNAPTTH	.....A.A.....G.....A.....C.....A.....	2170
MAJORITY	CCCTCTTCGGCCGCGGCTACGTGCCCCGACCTCAACGCCCGGTGAAGAGCGTGCGGGAGGCGGCGGA	
DNAPTAQ	.....C.....A.....AG.G.....C...	2234
DNAPTFL	.....T.....C.....	2231
DNAPTTH	.....AA.AA.....CA.....C.....	2240
MAJORITY	GCGCATGGCCTTCAACATGCCCCGTCCAGGGCACCGCCGCGACCTCATGAAGCTGGCCATGGTGAAGCTC	
DNAPTAQ	.....G.....T.....	2304
DNAPTFL	.....G.....CG...T	2301
DNAPTTH	.....C.....	2310
MAJORITY	TTCCCCCGGCTXCAGGAAATGGGGGCCAGGATGCTCCTXCAGGTCCACGACGAGCTGGTCTCGAGGCCCC	
DNAPTAQ	.....A...GG.....T.....	2374
DNAPTFL	.....T.....C.....G.....TT.G.....G.....	2371
DNAPTTH	.....C.C.G...G.....C.C.....C.....G.....	2380
MAJORITY	CCAAAGAGCGGGCGGAGGXGGTGGCCCGCTTTGGCCAAGGAGGTTCATGGAGGGGTCTATCCCCCTGGCCGT	
DNAPTAQ	A.....A.....CC.....CGGC.....G.....	2444
DNAPTFL	...G.C.....AG...A.....GG.....CAG..	2441
DNAPTTH	.C...C.....C...A.....G.....C.....AA..C.....C.....	2450

FIG. 2G



MAJORITY	GCCCCCTGGAGGTGGAGGTGGGGATGGGGGAGGAGTGGCTCTCCGCCCAAGGAGTAG	
DNAPTAQ	.....A.....	2499 GA
DNAPTFL	.....CC.....	2496
DNAPTTH	.....T.....GT...	2505

FIG. 2H

MAJORITY		MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEVPQAVYGFAKSLKALKEDG·DAVXVVVFDK	
TAD PRO	RG	.....H.....	69
TFL PRO		.....I.....	68
TTH PRO	E	.....V.V..... .....YK..F.....	70
MAJORITY		APSRHEAYEAYKAGRPTPEDFPROLALIKELVDLLGLXRLEVPGYEADDVLATLAKKAEKEGYEVRIL	
TAG PRO	GG	.....A.....S.....	139
TFL PRO		.....V.....F.....R.....	138
TTH PRO		.....FT.....	140
MAJORITY		TADRDLYQLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPNDLPGVKGIGECTAXKLLX	
TAG PRO	K	.....H.....D..A.....T..E.....R...E	209
TFL PRO	E	.....I.....Y.....A.....I.....QR..IR	208
TTH PRO	V	.....V.....H.....E.....F..V.....L...K	210
MAJORITY		EWGSLENLLKNLDRVKP·XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDREGLRAFLEF	
TAG PRO	A	.....L...AI...L...D..K..WD.AK.....K.....R.....	278
TFL PRO	FQH	.....Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL.....	277
TTH PRO		.....ENV...K..L...R..LE..R.....L.QG.....	280
MAJORITY		GSLLEFGLLXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEALLALAAARXGRVHRAXDPLXGLRDLKEV	
TAG PRO	S	.....S.....K.....D.....PE.YKA.....A	348
TFL PRO	G	.....A.....L..SF.....G.WE..L...Q...R.....G.	347
TTH PRO	A	.....A.AP.....K.....C.D.....A..A..K.....	350

**FIG. 3A**

MAJORITY		RGLLAKDLAVLALREGLDLXPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTE	DAGERALLSERLFXNLXX
TAQ PRO	.....S.....	G.P.....	E.....A.....A..WG 418
TFL PRO	..I.....	F.E.....	A.....QT.KE 417
TTH PRO	.....S.....	V.....	AH.....HR..LK 420
MAJORITY		RLEGEERLLWLXYEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRLEE	VFRLAGHPFNLNSRD
TAQ PRO	.....R...R...A.....	R.....A.....A.....	488
TFL PRO	..K.....E.....	R.....EA.V.Q.....	487
TTH PRO	.....K.....H.....	L.....L.....	490
MAJORITY		QLERVLFDELGLPAIGKTEKTKGRSTSAAVLEALREAHPIVEKILQYRELTKL	KNTYIDPLPXLVHPRTG
TAQ PRO0	.....	.....	S.....D.I..... 558
TFL PRO	.....	DR.....	A.....K.. 557
TTH PRO	.....R...L...Q.....	H.....V.....S.....	560
MAJORITY		RLHTRFNQTATATGRLSSSDPNLQNIPTPLGQRIRRAFVAEEGWXLVALDYSQ	IELRVLAHLSGDENL
TAQ PRO	.....	I.....L.....	628
TFL PRO	.....	V.V.....	627
TTH PRO	.....	A.A.....	630
MAJORITY		IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVL YGMSAHRLSQ	ELAIPIYEEAVAFIERYFQ
TAQ PRO	.....E.....	R.....	Q..... 698
TFL PRO	.....S.G.....	G.S.....	697
TTH PRO	.....K.....	V.....	700

FIG. 3B

MAJORITY	SFPKVR	AWIEKT	LEEGR	RRGY	VETLF	GRRR	YVPDL	NARV	KSVRE	AAERMA	FNPV	QGTAA	DL	MKLAM	VKL	
TAQ PRO	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	768
TFL PRO	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	767
TTH PRO	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	770

MAJORITY	FPRLX	EMGAR	MLLQ	VHDEL	VLEAP	KXRA	EXVA	ALAKE	VM	EGVY	PLAV	PLEVE	VGXG	EDWL	SAKEX	
TAQ PRO	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	833
TFL PRO	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	831
TTH PRO	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	835

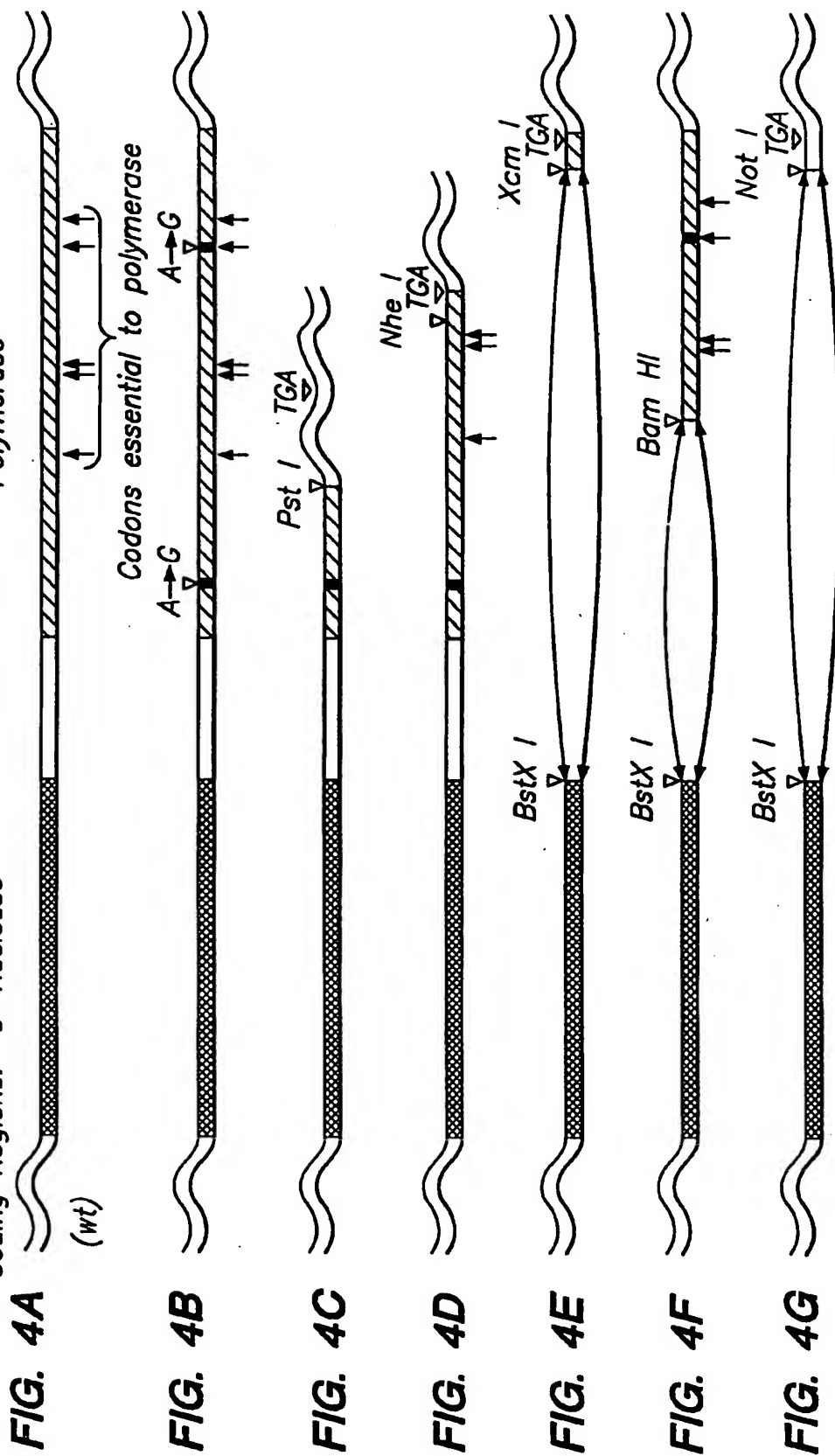
FIG. 3C

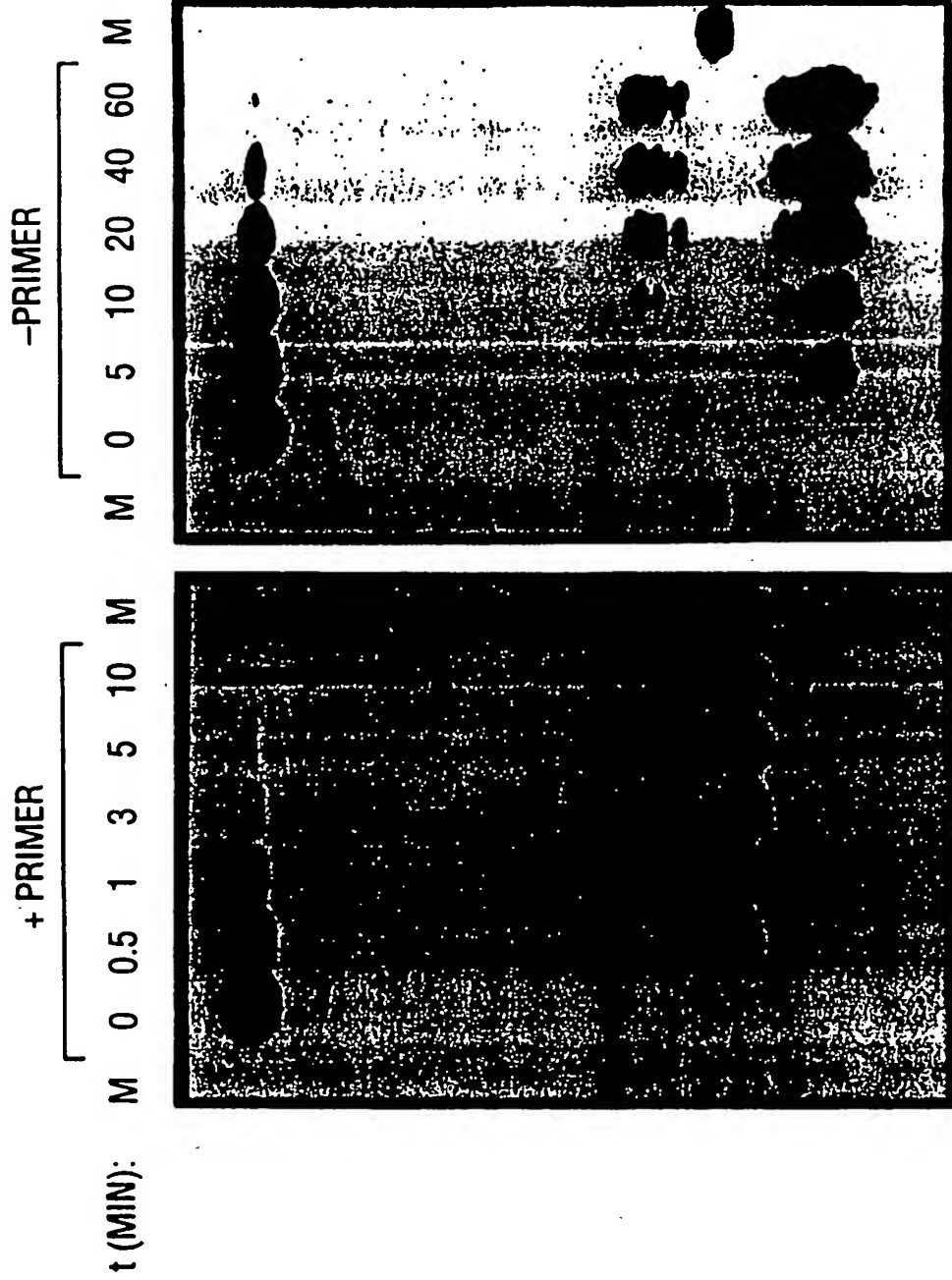
Genes for Wild-Type and Pol(-)DNAPTaq

Domain

Coding Regions: 5' Nuclease

Polymerase





**FIG. 10A**

**FIG. 10B**

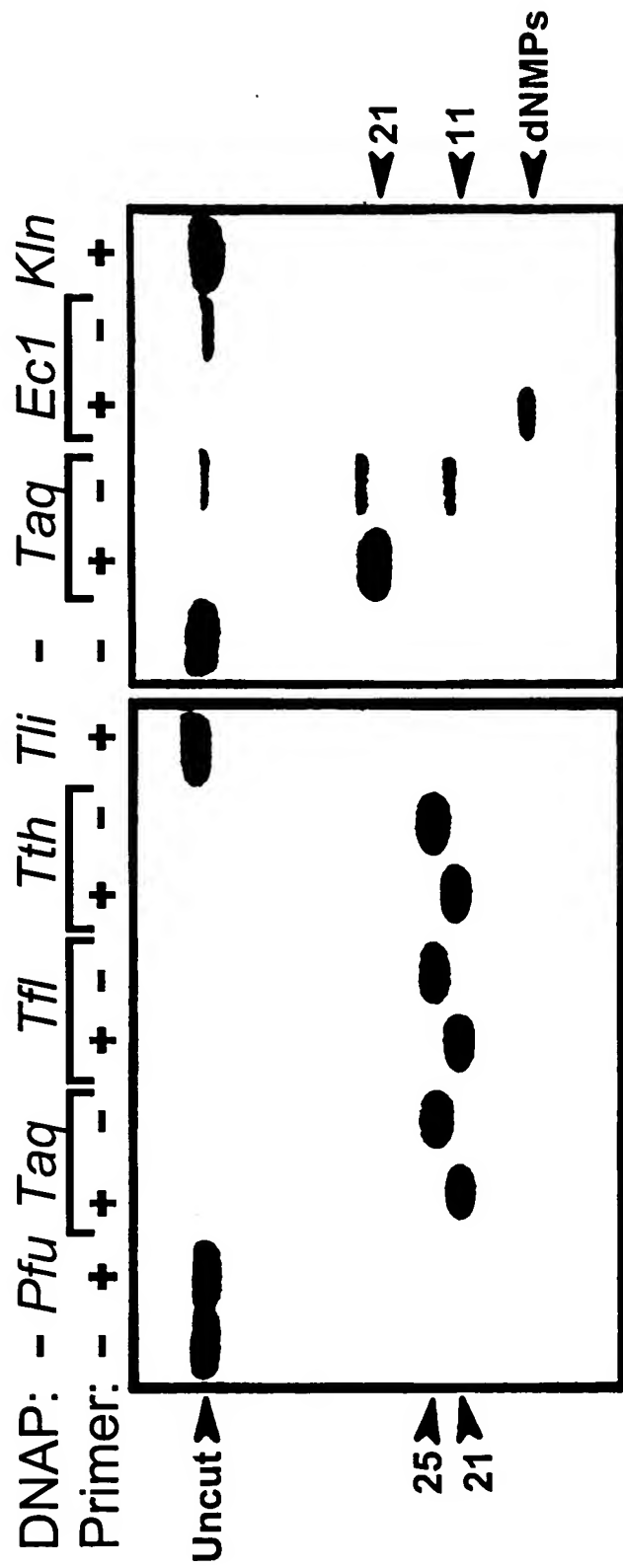
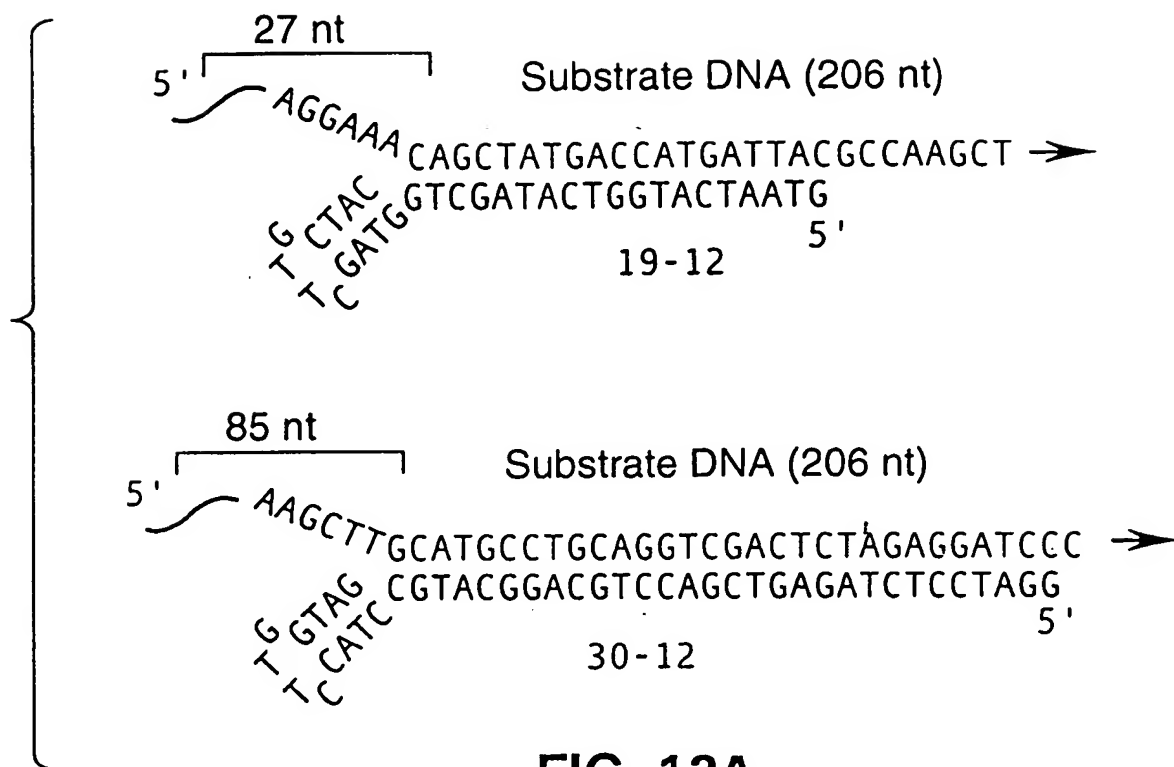
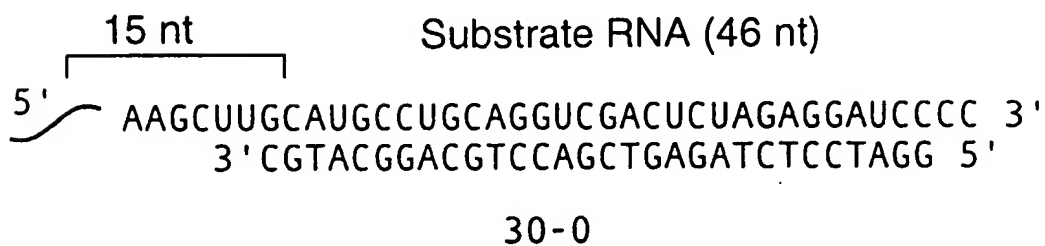


FIG. 11A

FIG. 11B

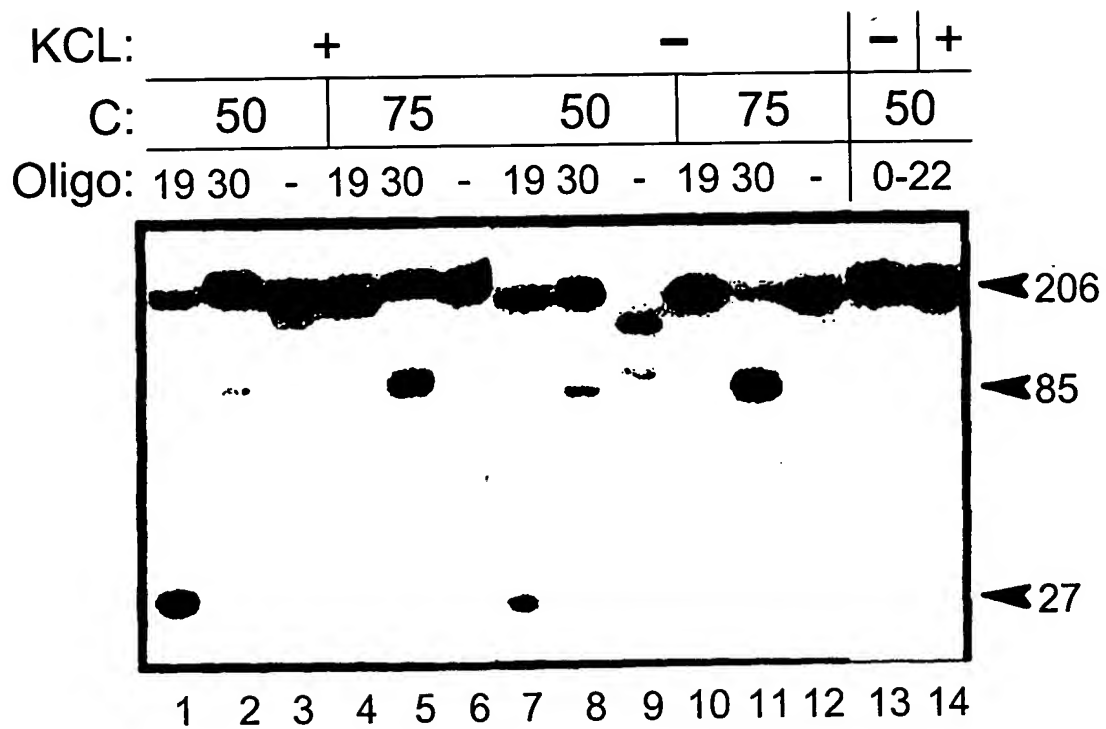


**FIG. 12A**

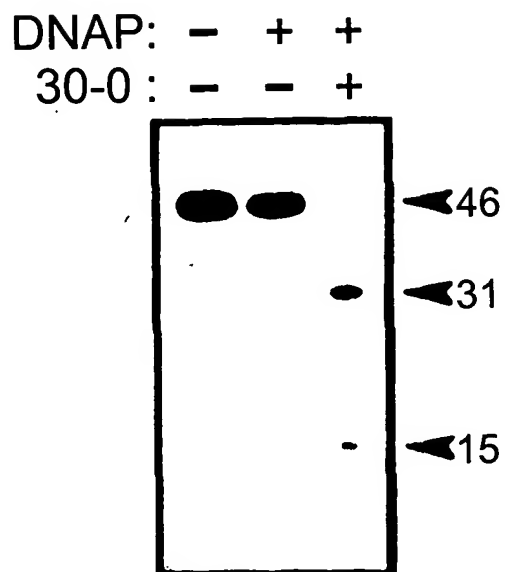


**FIG. 13A**



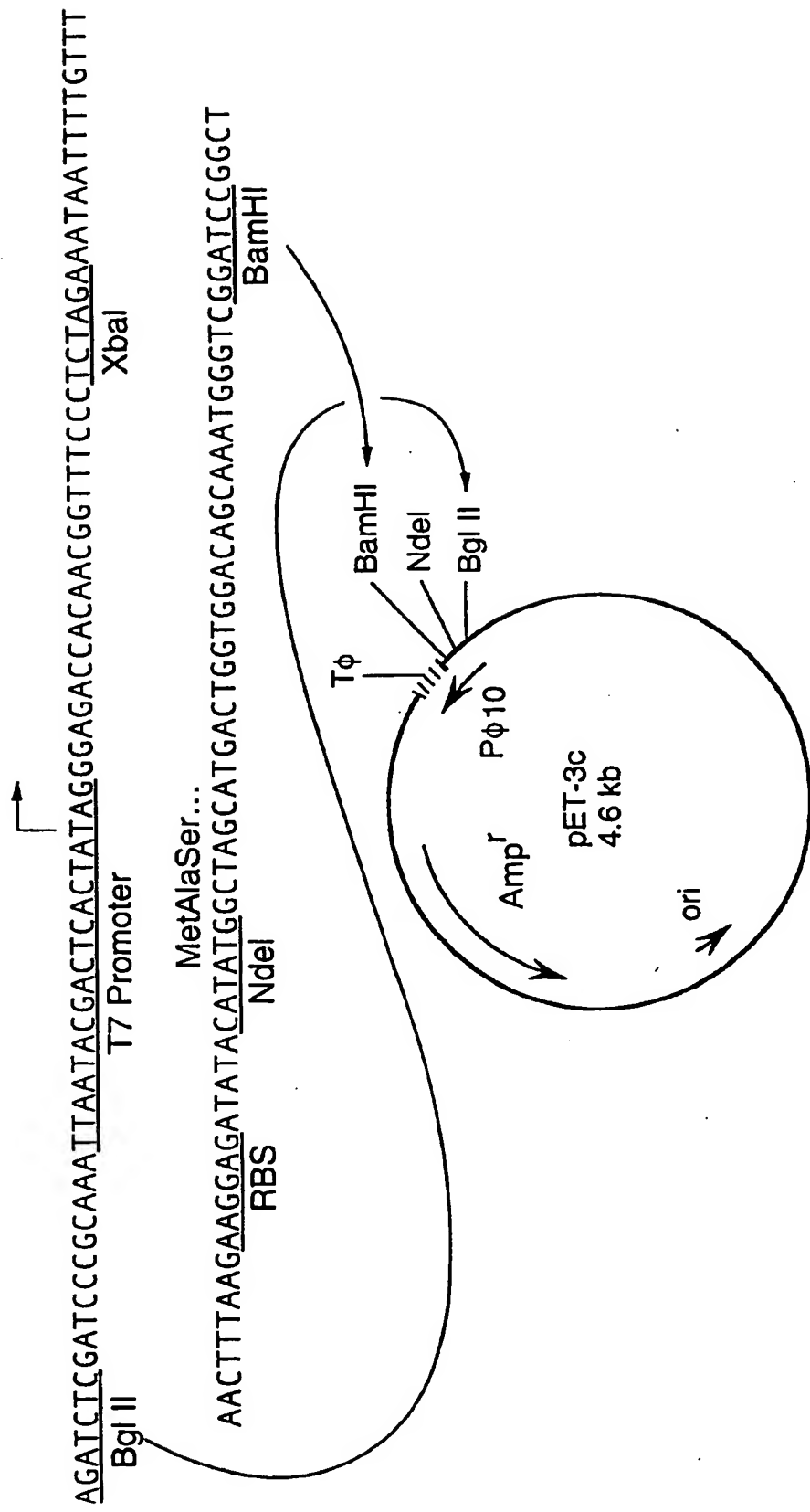


**FIG. 12B**



**FIG. 13B**





P $\phi$ 10: Bacteriophage T7  $\phi$ 10 promoter    RBS: Ribosome binding site  
T $\phi$ : T7  $\phi$  Terminator

**FIG. 15**



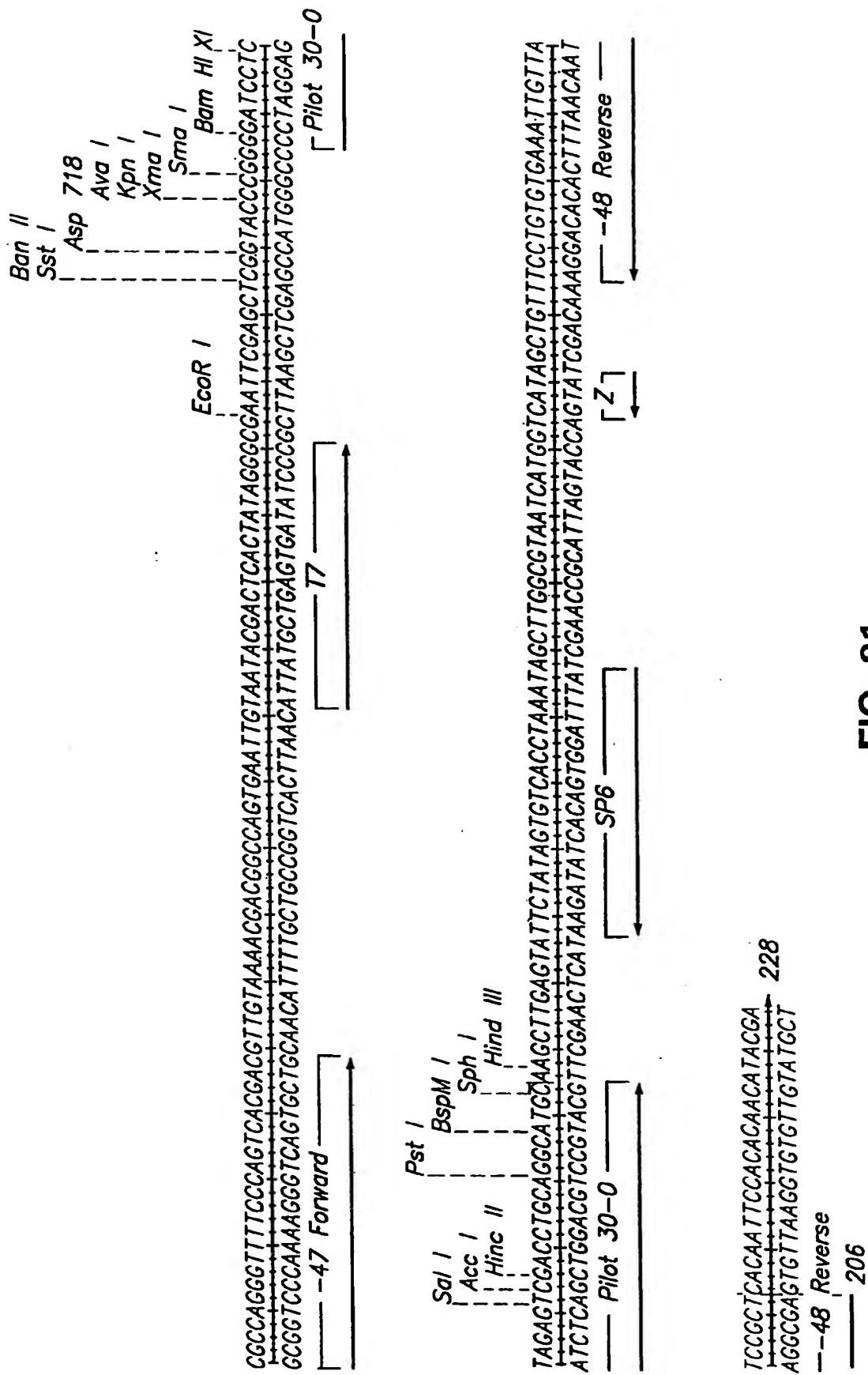
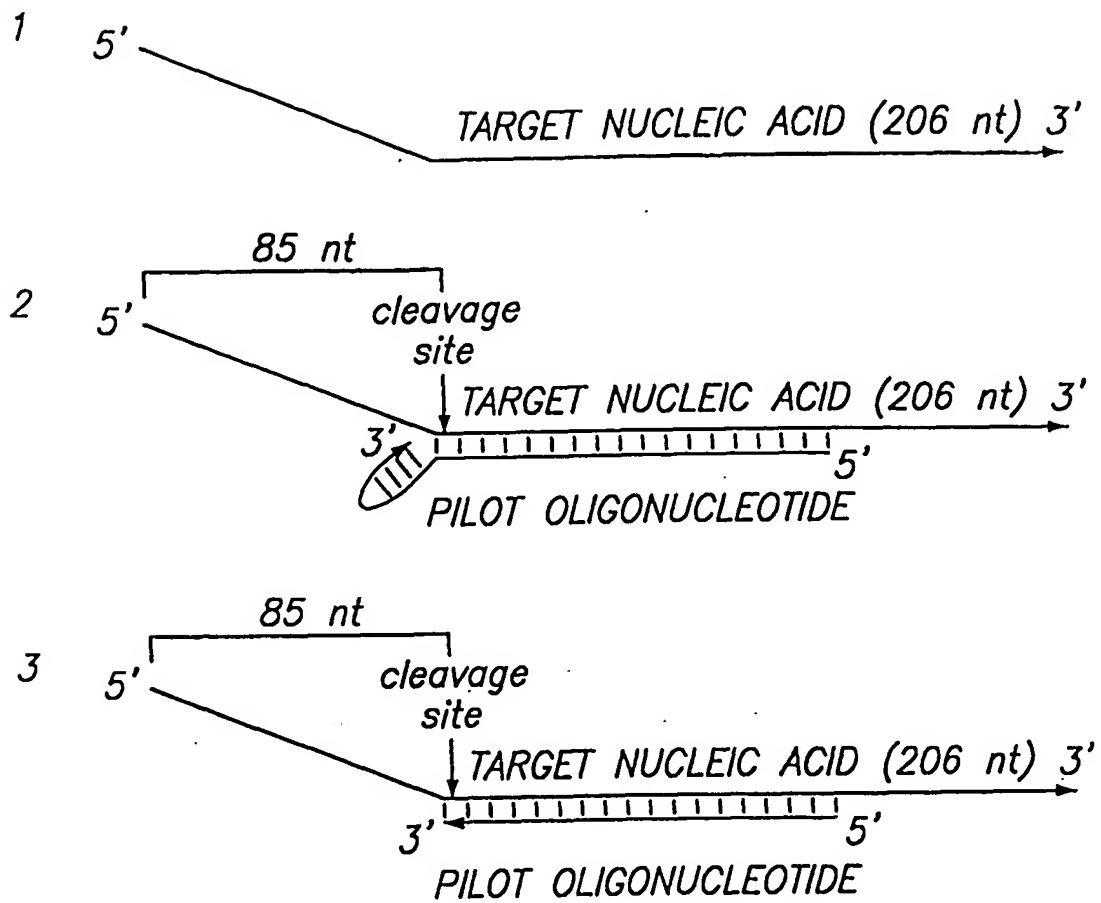


FIG. 21



**FIG. 22A**

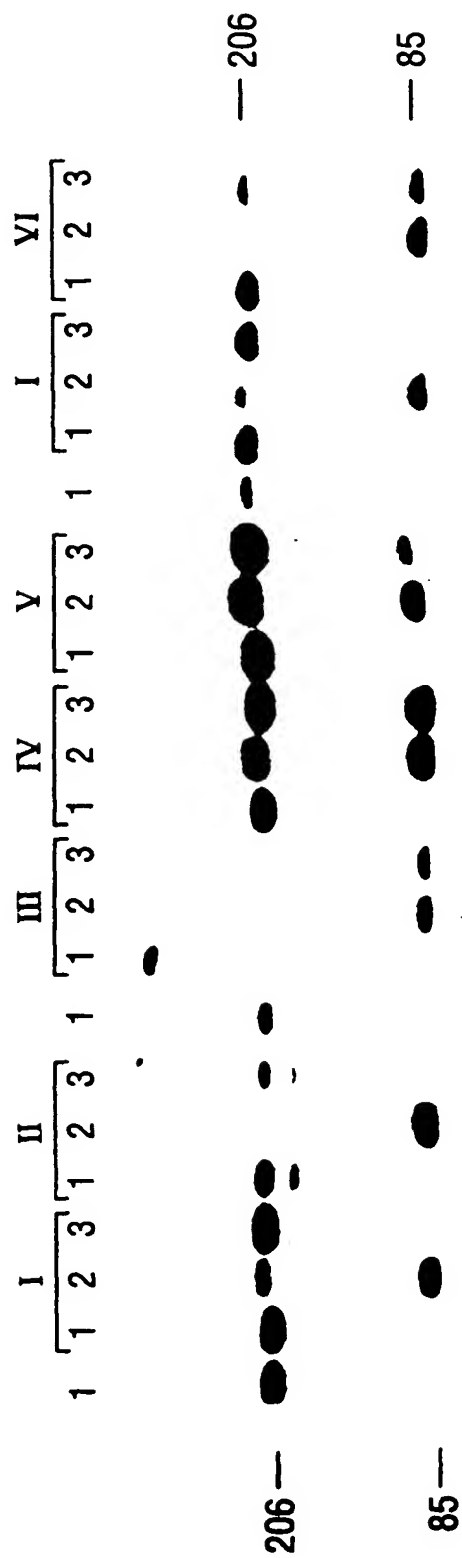


FIG. 22B

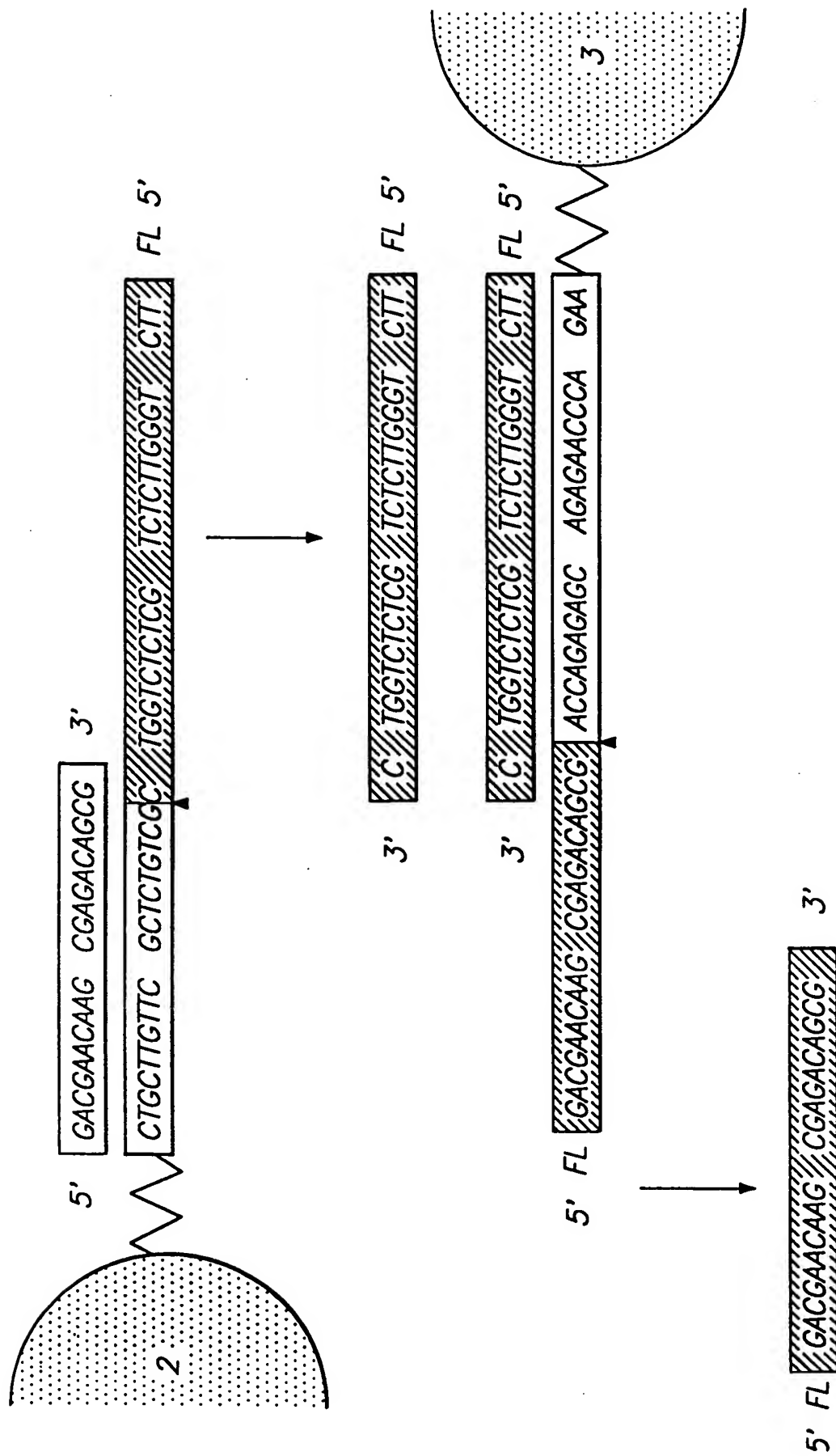


FIG. 23



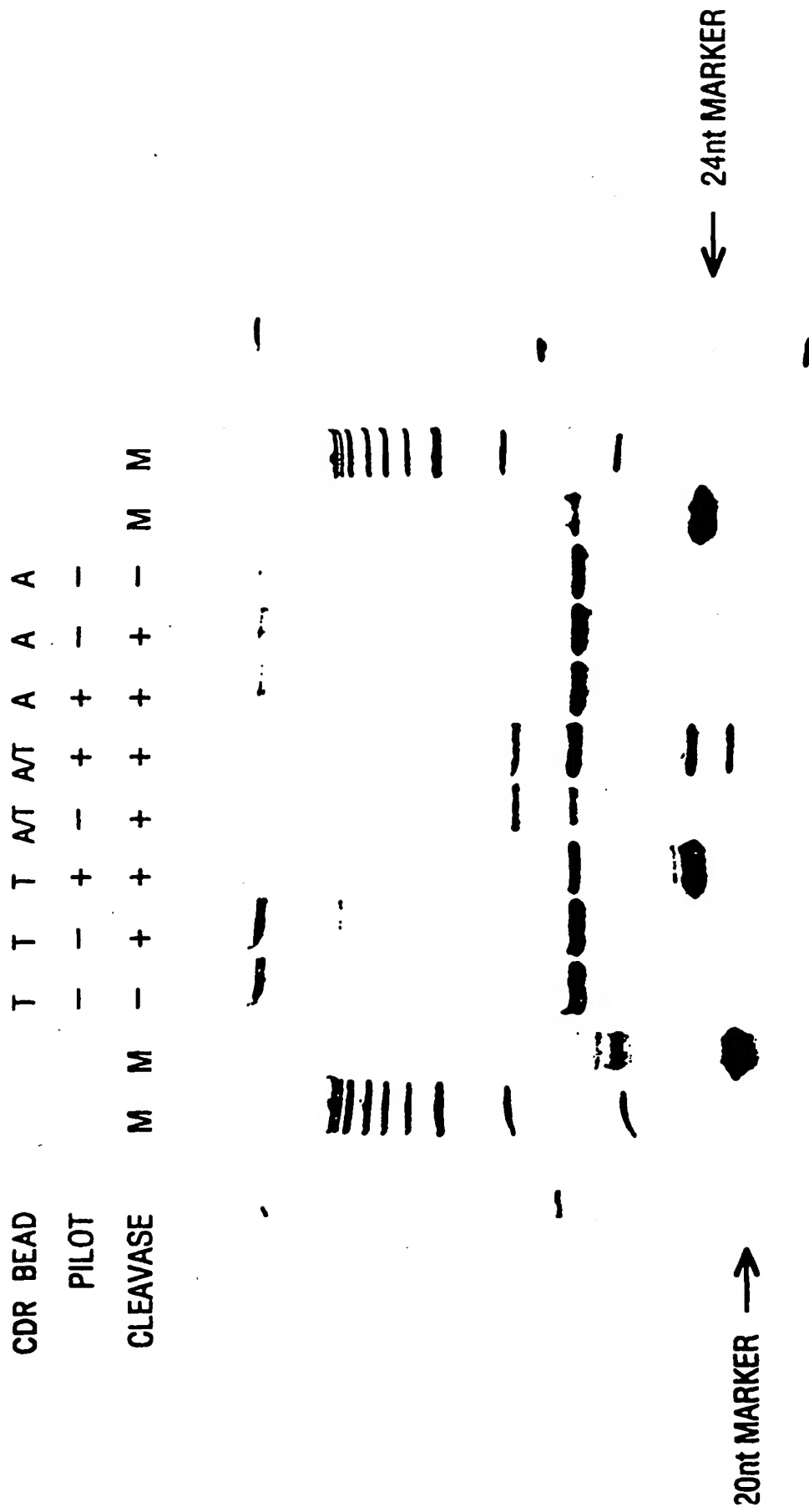
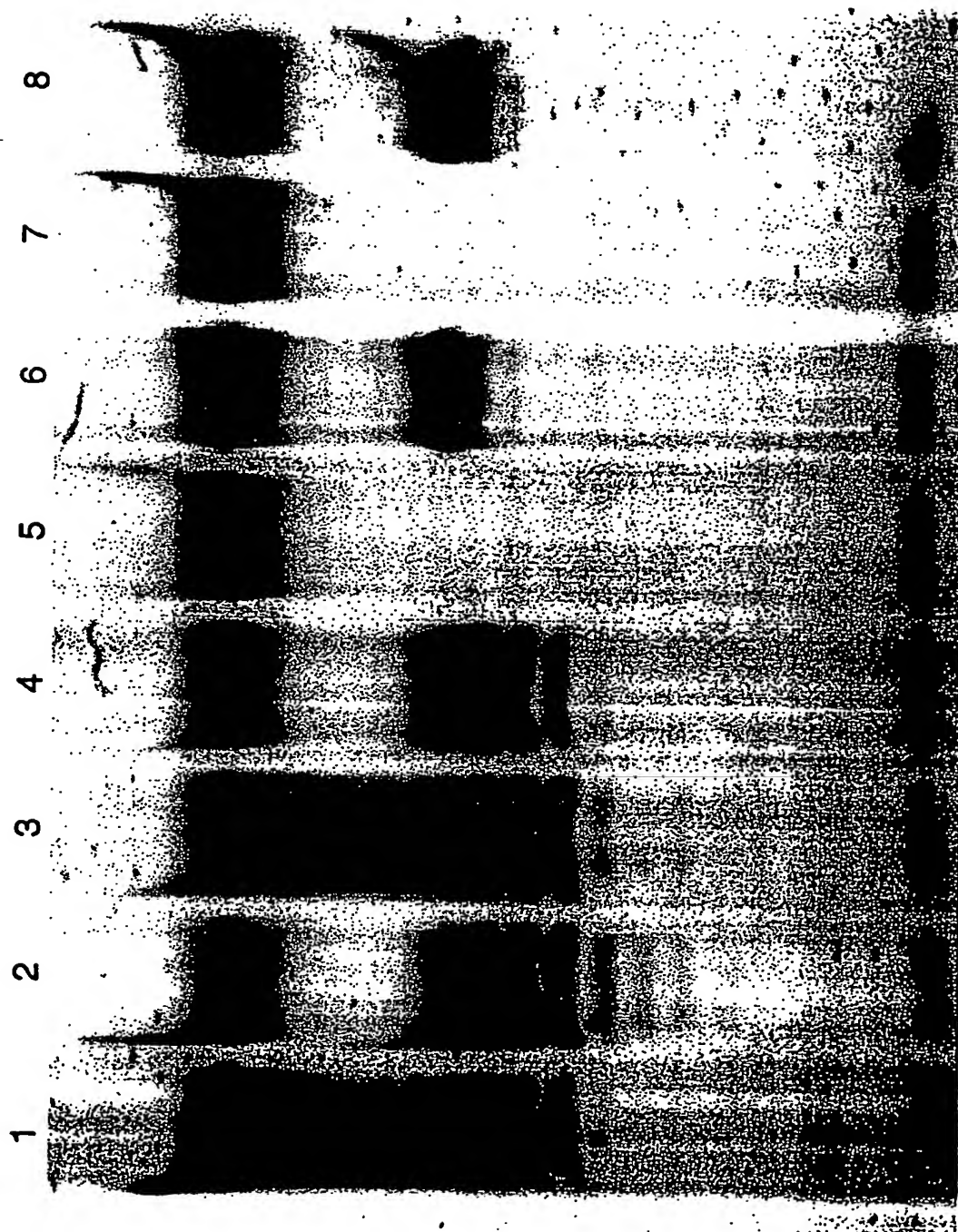


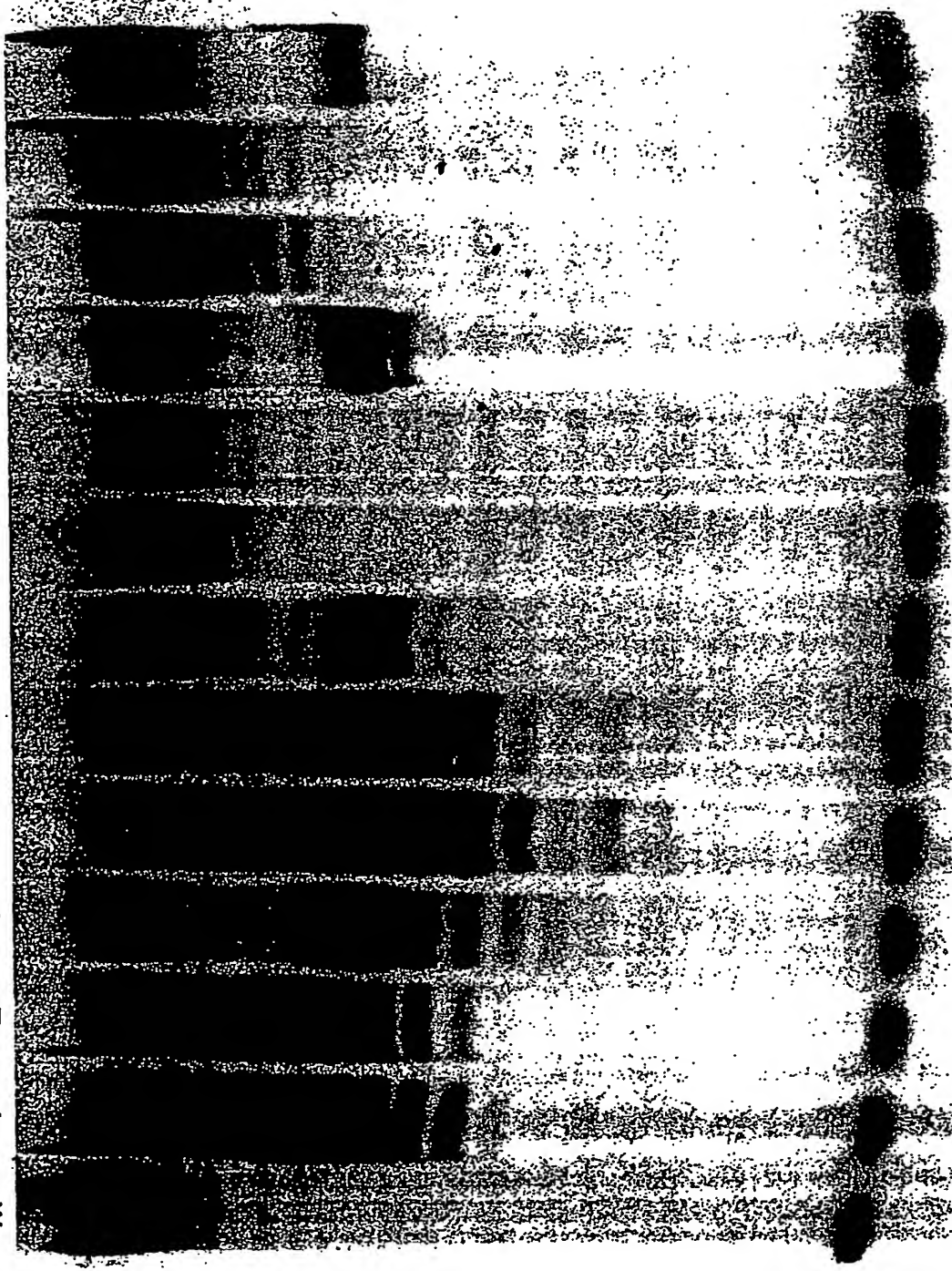
FIG. 24



26

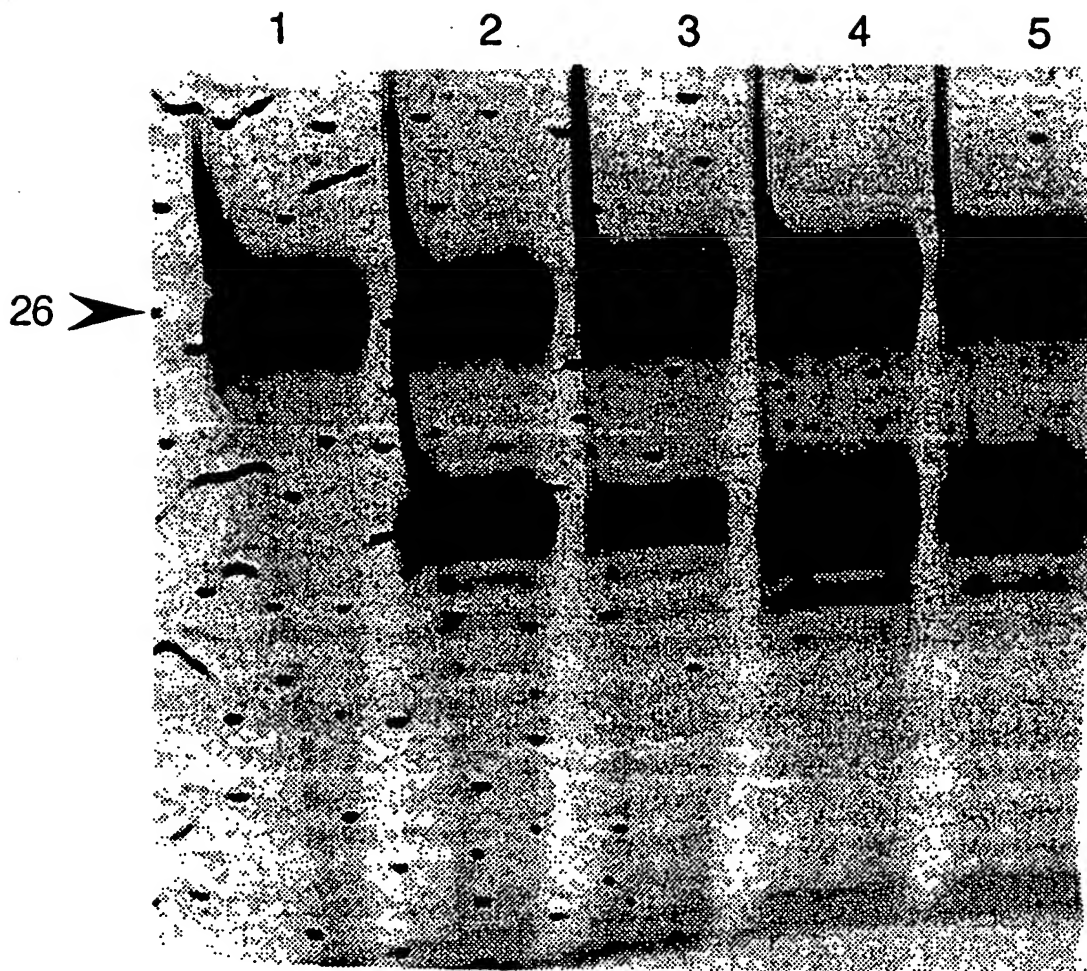
FIG. 33

M 1 2 3 4 5 6 7 8 9 10 11 12



26

FIG. 34



**FIG. 35**

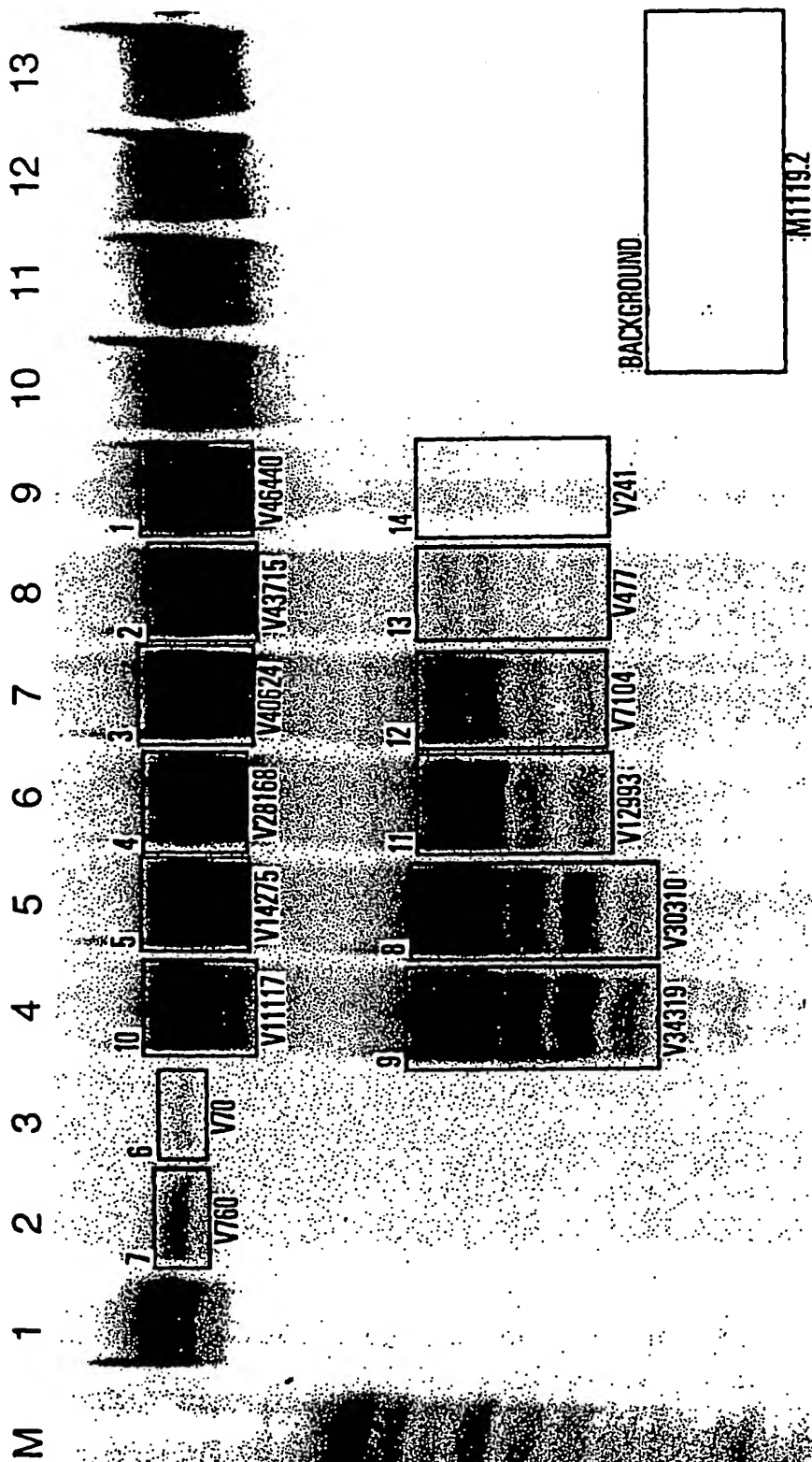


FIG. 36

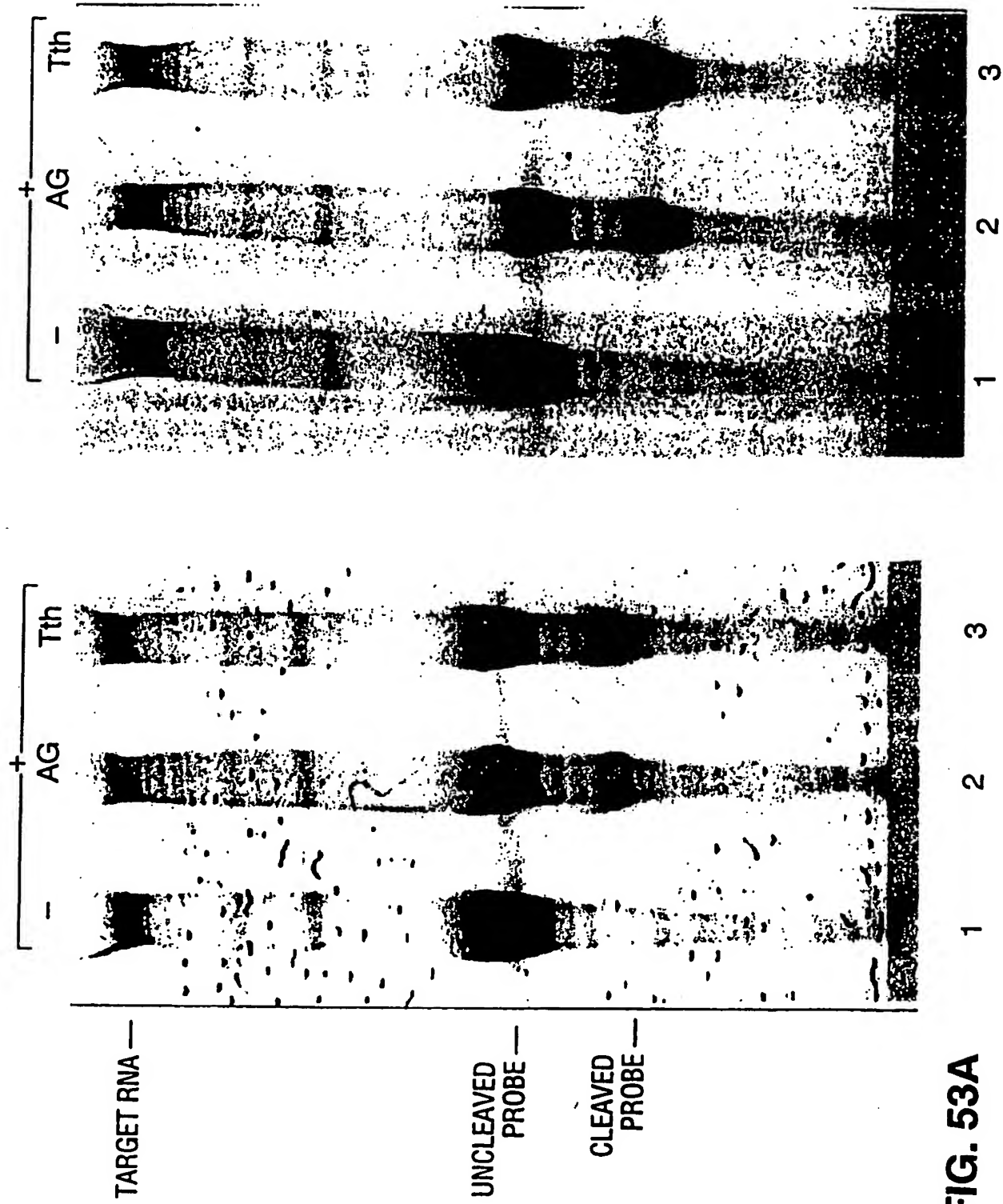
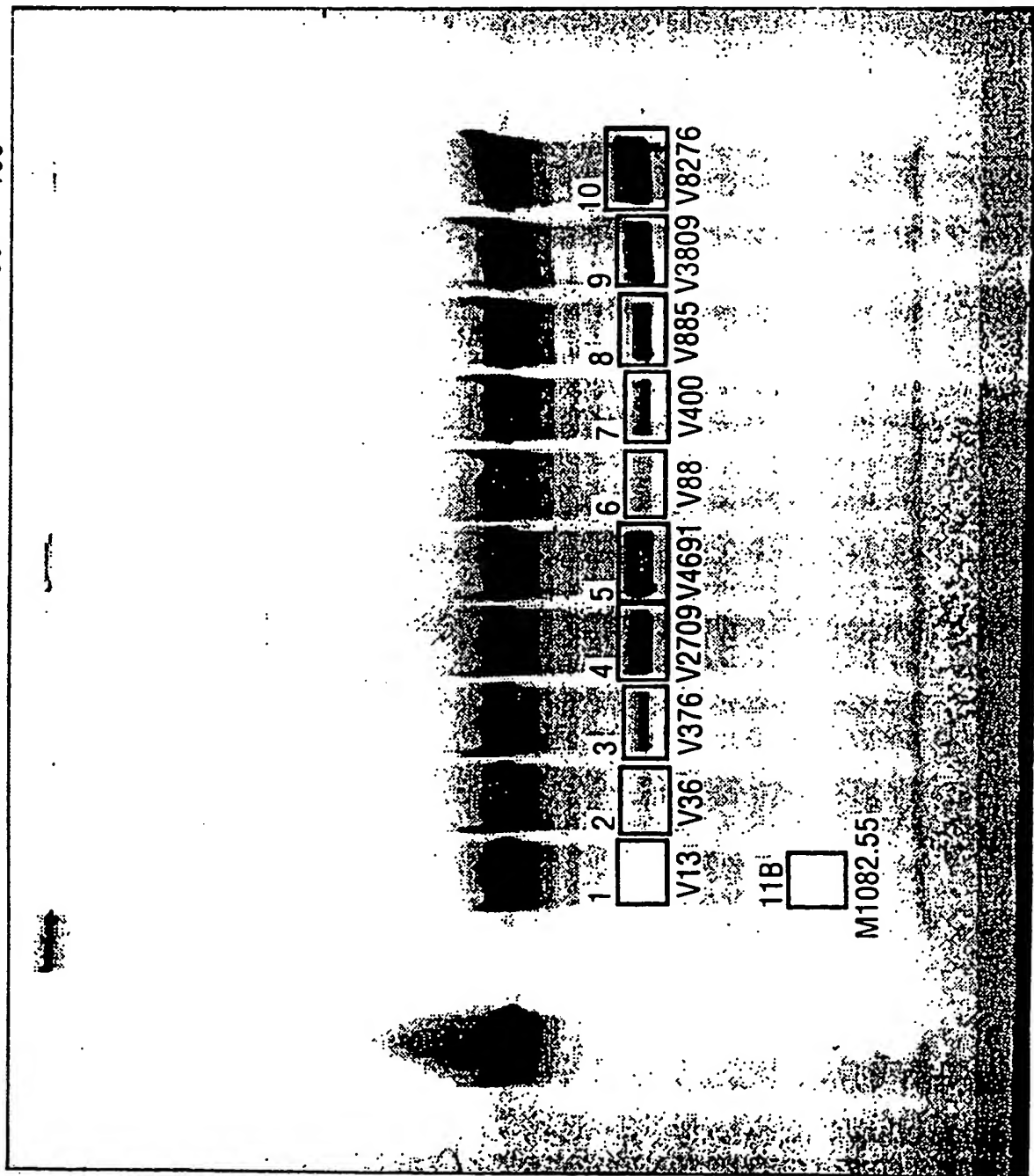


FIG. 53A

FIG. 53B

— ENZYME  
— TARGET (fmol)  
— RNA

CLEAVASE AG 100 50 10 5 1 500 100 50 10 5 1 100 50 10 5 1 100



— PROBE

— PRODUCT

FIG. 54

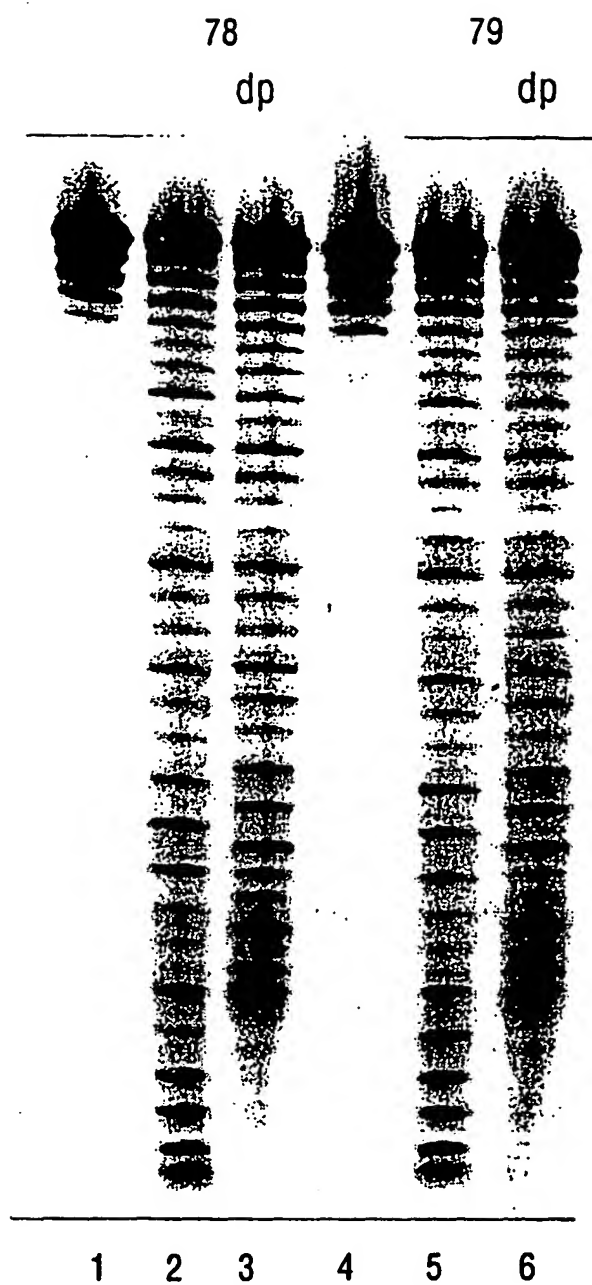


FIG. 55



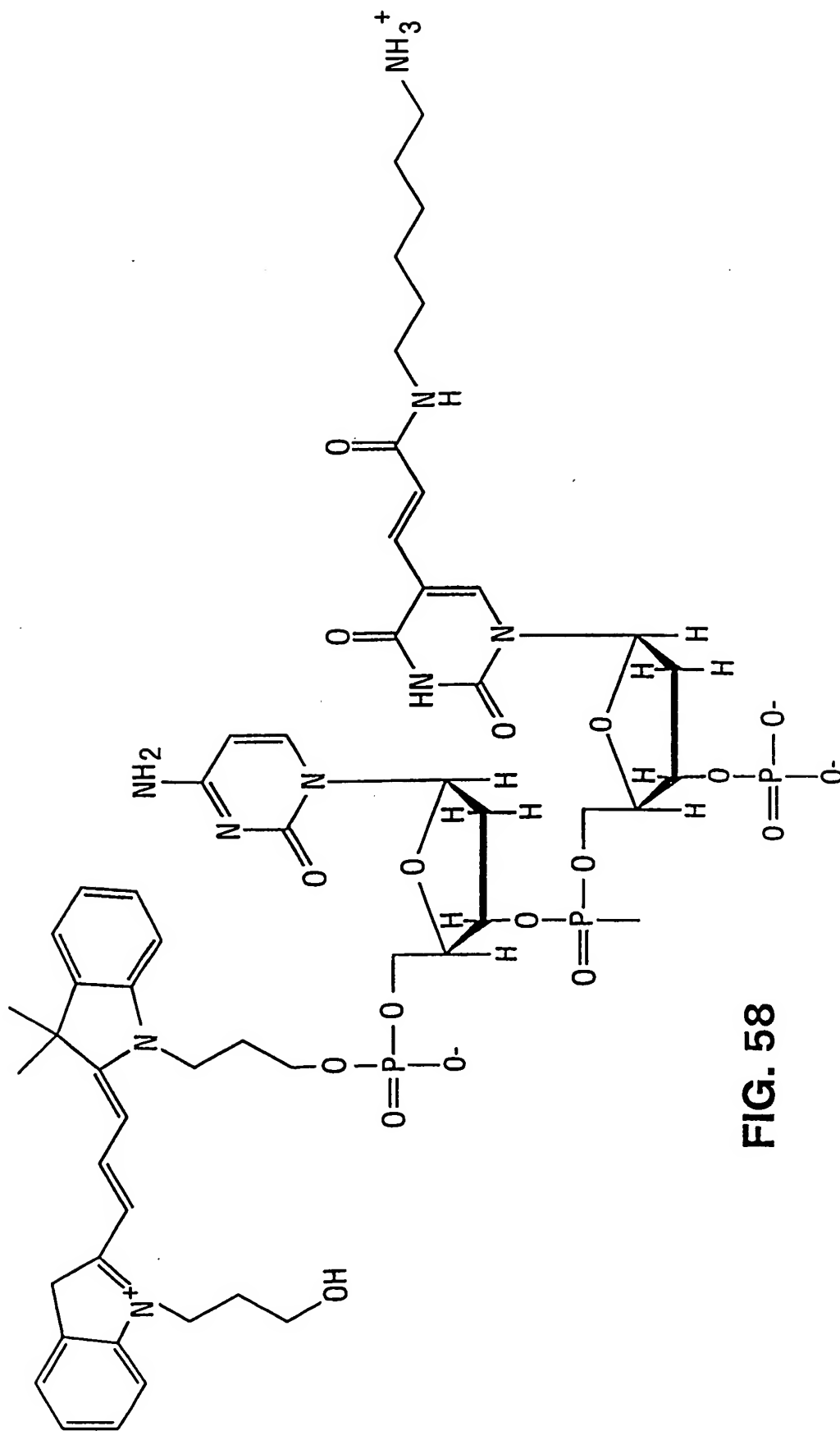




FIG. 65A

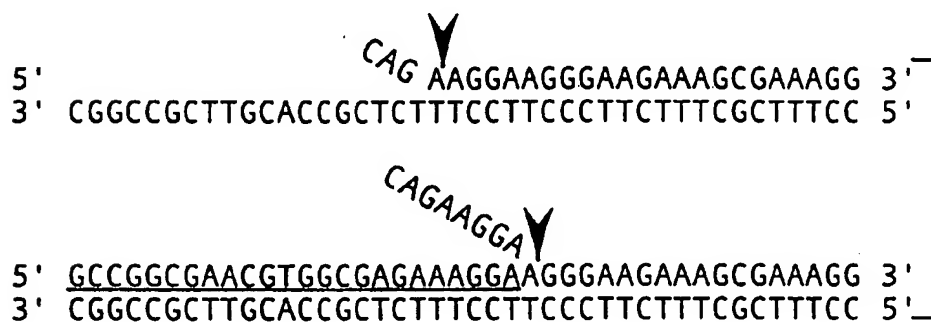


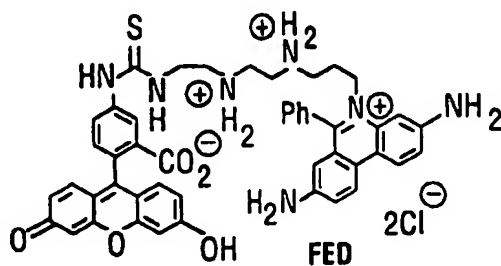
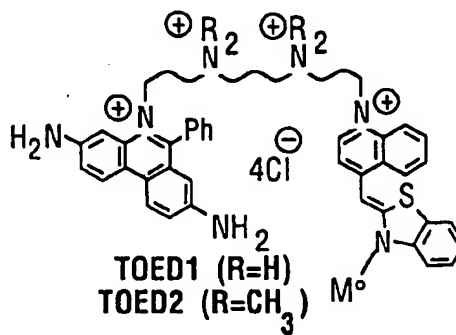
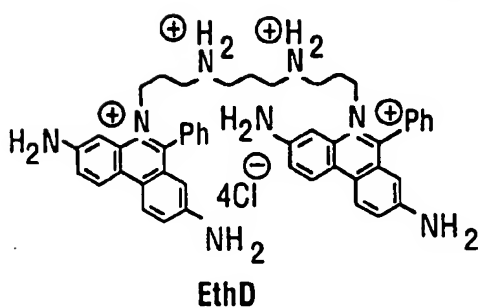
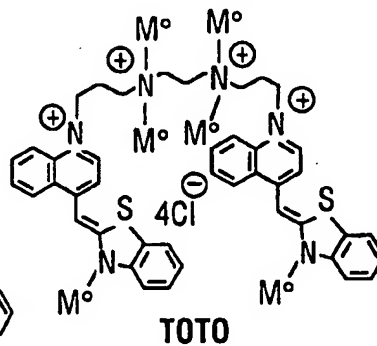
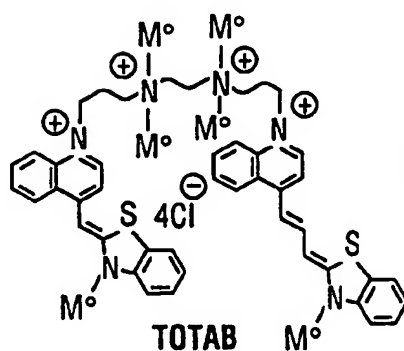
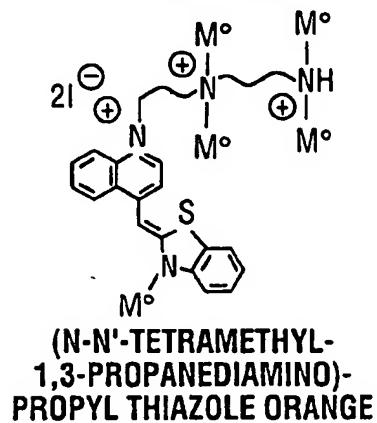
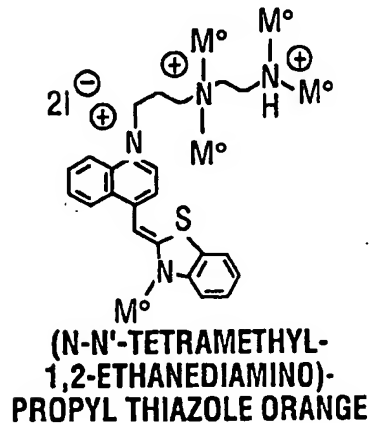
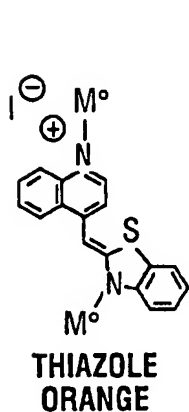
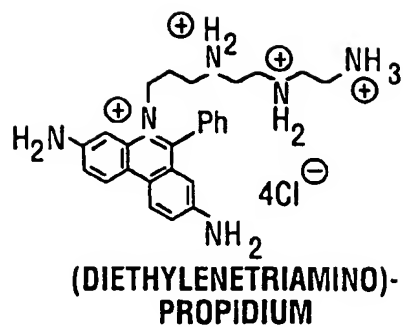
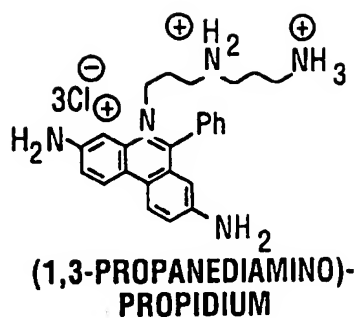
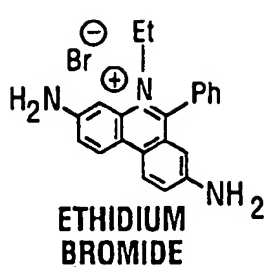
FIG. 65B



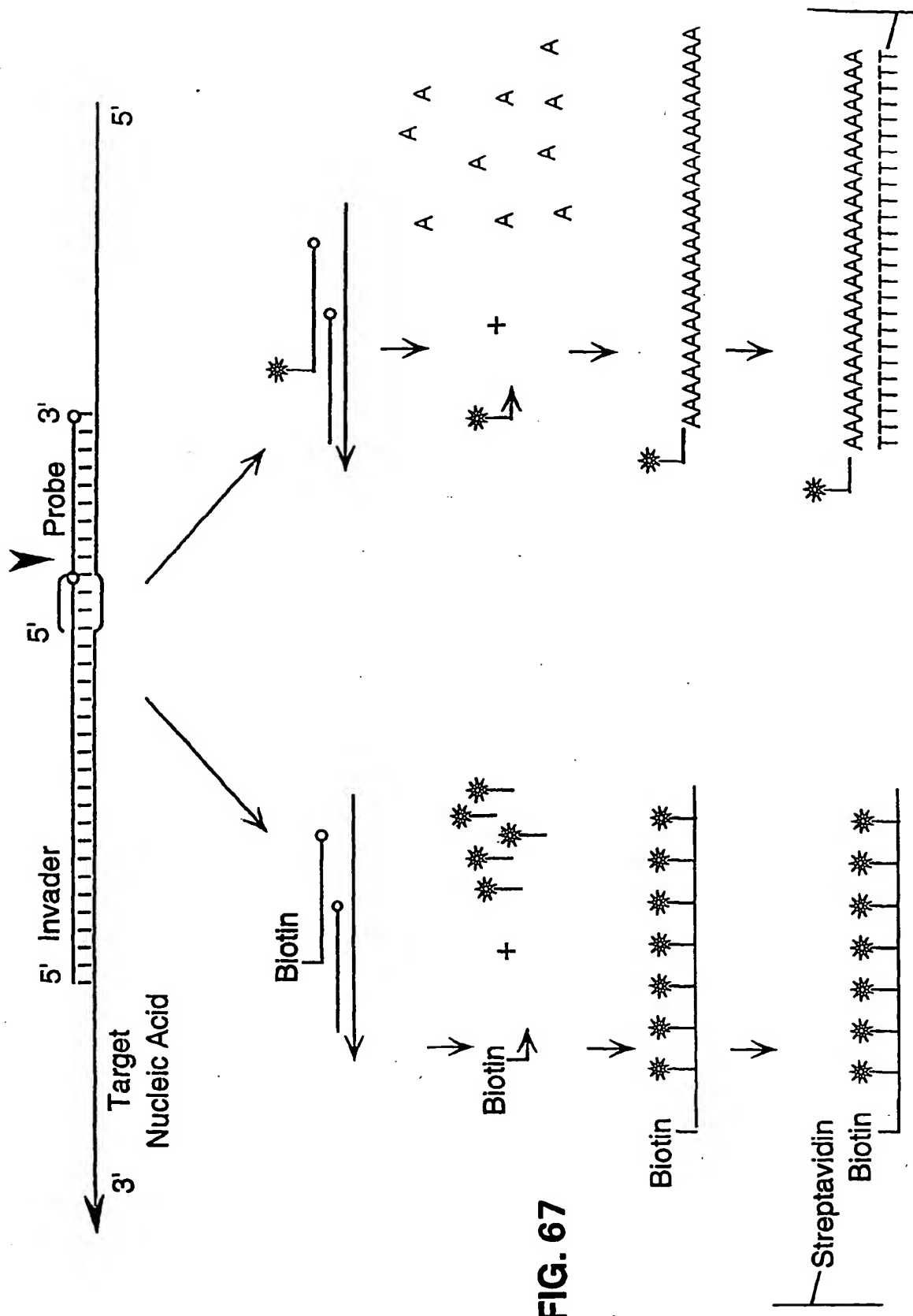
FIG. 65C

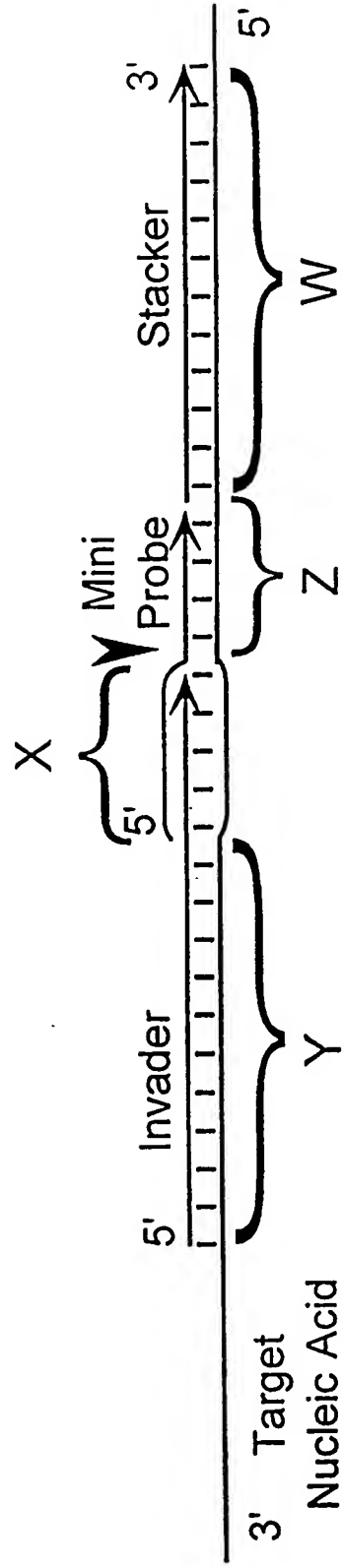


FIG. 65D



**FIG. 66**





**FIG. 68**

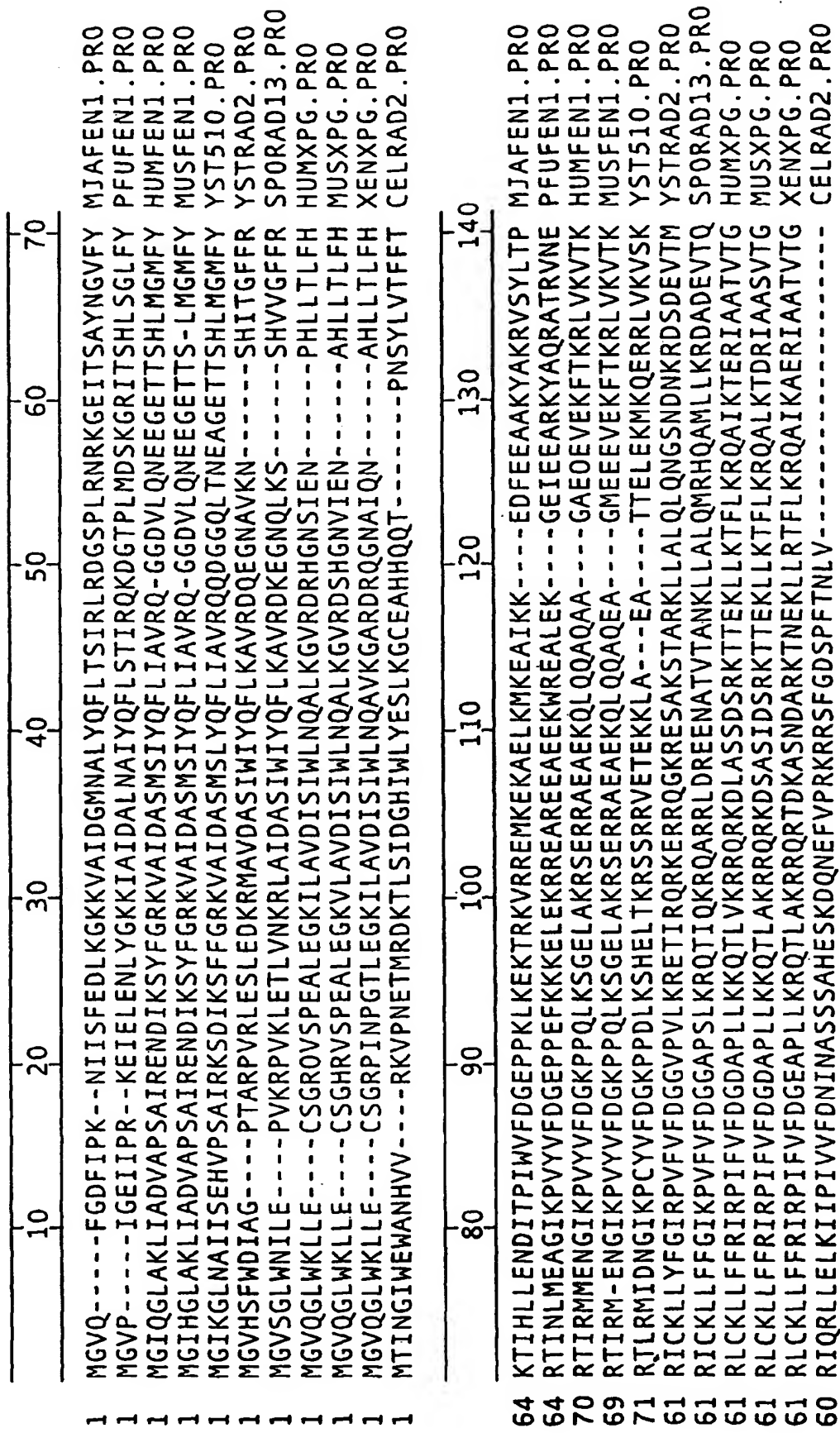


FIG. 70A

	150	160	170	180	190	200	210
130	KMVENCKYLLSLMGIPYVEAPSEGEAQASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLT	TTTKEM----					MJAFEN1.PRO
130	MLIEDAKKLLLELMGIPYVQAPSEGEAQAAAYMAAKGSVYASASQDYDSLFLGAPRLVRNLT	ITGKRKLPGK					PFUFEN1.PRO
136	QHNDECKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLT	ASEAKKLP IQ					HUMFEN1.PRO
134	QHNDECKHLLSLMGIPYLDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHLT	ASEAKKLP IQ					MUSFEN1.PRO
134	EHNEEAQKLLGLMGIPYIIAPTEAEQAQCAELAKKGKVYAAASEMDTLCYRTPFLLRHLT	FSEAKKEPIH					YST510.PRO
131	DMIKEVQELLSRFGIPYITAPMEAEQAQCAELLQLNLVDGIITDDSDVFLFGGKIYKNMF	HEKNY----					YSTRAD2.PRO
131	VMIKECQELRLFGIPYIVAPOEAEQAQCSKLELKLVDGIVTDDSDVFLFGGTRVYRNMF	NQNF----					SPORAD13.PRO
131	QMFLESQELRLFGIPYIQAPMEAEQAQCAILDLDQTSGTITDDSDIWLFGARHVYRNFF	NKNKF----					HUMXPG.PRO
131	QMFLESQELRLFGVPYIQAPMEAEAOCAVLDSLQTSGTITDDSDIWLFGARHVYKNFF	NKNKF----					MUSXPG.PRO
131	QMCLESQELQLFGIPYIVAPMEAEQAQCAILDLDQTSGTITDDSDIWLFGARHVYKNFF	SQNKH----					XENXPG.PRO
111	DHVYKTNALLTELGIKVIAPGDGEAQCARLEQLGVTSGCITTDFDYFLFGGKNLYRFD	TAGT-----					CELRAD2.PRO

	220	230	240	250	260	270	280
195	-----PELIELNEVLEDLRISLDDLIDIAIFMGTDYNPGGV--K--GIGKRAYELVRSGVAK--DV						MJAFEN1.PRO
200	NVYVE-IKPELIILEEVLKELKLTREKLIELAILVGTDYNPGGI--K--GIGLKKALEIVRHSKDPLAKF						PFUFEN1.PRO
206	EFHLSRILQELGLNQEVDLCIILGSDYCESIRGIGPKRAVDLIQK--HKSIEEIVRRLDPN-----KY						HUMFEN1.PRO
204	EFHLSRVLQELGLNQEVDLCIILGSDYCESIRGIGAKRAVDLIQK--HKSIEEIVRRLDPS-----KY						MUSFEN1.PRO
204	EIDTELVLRGDLTIEQFVDLCIMLGCDYCESIRGVGPVTALKLIKT--HGSIEKIVEFIESGESNNTKW						YST510.PRO
198	FYDAESILKLLGLDRKNMIELAQLGSDYTNGLKGMPVSSIEVIAEF--GNLKNFKDWYNNNGOFDKRK						YSTRAD2.PRO
198	LYLMDDMKREFNVNQMDLIKLAHLGSDYTMGLSRVGPVLALEILHEFPDGTGLFEFKKWFQRLSTGHAS						SPORAD13.PRO
198	YYQYVDFHNLGLDRNKLINLAYLLGSDYTEGIPYVGCVTAMEILNEFPFGHGLEPLLKFESEWHEAQKNP						HUMXPG.PRO
119	YYQYVDFYSQLGLDRNKLINLAYLLGSDYTEGIPYVGCVTAMEILNEFPGRGLDPLLKFESEWHEAQNNK						MUSXPG.PRO
198	YYQYADIHNOLGLDRSKLINLAYLLGSDYTEGIPYVGSAMEILNEFPQGQGLEPLVKFEKWSEAQKDK						XENXPG.PRO
175	-----SSTACLHDIMHLSLGRMFM-----						CELRAD2.PRO

FIG. 70B

	290	300	310	320	330	340	350
251	LKKEVEYYDEIKRIFKEPKV-----	TD--	NYSLSLKLDPKEGIIFLVDENDFN	YD	MJAFEN1.PRO		
265	QKQSDVDLYAIKEFFLNPPV-----	TD--	NYNLVWRDPDEEGILKFLCDEHDFSEE		PFUFEN1.PRO		
269	PVPENWLHKEAHQLFLEPEV-----	LDPE	SVELKWSEPNNEELIKFMCGEKQFSEE		HUMFEN1.PRO		
267	PVPENWLHKEAQLFLEPEV-----	VDPE	SVELKWSEPNNEELVKFMCGEKQFSEE		MUSFEN1.PRO		
272	KIPEDWPYKQARMFLDPEV-----	IDGNE	INLKWSPKKEKELIEYLCDDKKFSEE		YST510.PRO		
265	QETENKFEKDLRKKLVNNEIILDDDFPSVMVYDAYMRPEVDHDTTPFVWGVDPDLMLRSFMKTQLGWPHE				YSTRAD2.PRO		
268	KNDVNTPVKKRINKLVGK-IILPSEFPNPLVDEAYLHPAVDDSKQSFQWGI	PDLD	DEL	RQFLMATVGWSKQ	SPORAD13.PRO		
268	KIRPNPHDTKVKKKL--RTLQLTPGFNPAPAAEAYLKPVVDDSKGSFLWGKPDLDKIREFCQRYFGWNR	T			HUMXPG.PRO		
268	KVAENPYDTKVKKKL--RKLQLTPGFNPAPADAYLRPVVDDSRGSFLWGKPDVDKIREFCORYFGWNR	M			MUSXPG.PRO		
268	KMRPNPNDTKVKKKL--RLDLQQSFPNPAPASAYLKPVVDESKSAFSWGRPDLEQIREFCESRFGWYRL				XENXPG.PRO		
194	-----EKKVSRPHLIS	TAIL	LGCDYFORGVQNI	GIVSVF	-ILGEFGDDGNEEIDPHVILDRFASYVRE	CELRAD2.PRO	
	360	370	380	390	400	410	420
300	RVKKHVVDKLYNLIA-----						MJAFEN1.PRO
314	RVKNGLERLKKAI-----						PFUFEN1.PRO
320	RIRSGVKRLSKSRQGS-TQGRLLDDFFKVT-----						HUMFEN1.PRO
318	RIRSGVKRLSKSRQGS-TQGRLLDDFFKVT-----						MUSFEN1.PRO
323	RVKSGISRLKKGLKSG-IQGRLLDGFFOVV-----						YST510.PRO
335	KSDEILIPLIIRDVNRKK-----						YSTRAD2.PRO
337	RTNEVLLPVIQDMHKKOF-----						SPORAD13.PRO
336	KTDESLLFPVLKQLDAQQTQLRIDSFFRLAQQEKEDAKRIKSQRLNRAVTCMLRKEKEAAASEIEAVSVAM						HUMXPG.PRO
336	KTDESLLPVLKHLNAHQTLRIDSFFRLAQQEKQDAKLKSHRLSRAVTCMLRKEEREKAPELTKVTEAM						MUSXPG.PRO
336	KTDEVLLPVLKQLNAQQTQLRIDSFFRLAQQEKQDAKLKSHRLSRAVTCMLRKEEREKAPELTKVTEAM						XENXPG.PRO
257	EIPARSED	TQRKLR	LRKKYN	FPVGF	PNCD	AVHNAITMYLR	PPVSSEIPKIIPR-----AANFQQVAEIM

FIG. 70C



	430	440	450	460	470	480	490
314	-----	-----	-----	-----	-----	-----	MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	PFUFEN1.PRO
348	-----	-----	-----	-----	-----	-----GSL	HUMFEN1.PRO
346	-----	-----	-----	-----	-----	-----GSL	MUSFEN1.PRO
351	-----	-----	-----	-----	-----	-----PK-T	YST510.PRO
357	KRINEFF	-----	-----	-----	-----	-----	YSTRAD2.PRO
359	SNLTQFFEGGNTN	VYAPRVAYHFKSKRL	ENALSSFKNQISNQSP	MSSEEIQADADA	FGESKGSDELO	SRI	SPORAD13.PRO
406	EKEFELLDKAKRKT	QKRGITNTLEESS	LKRRLSDSKRNT	CGGFLGETCL	SESSDGSSEHA	ESSLM	HUMXPG.PRO
406	EKEFELDDAKGKT	OKRELPYK-----	KETSVPKRRRPS	GNNGGFLGDPYC	SESPQESSCED	GEGSSVM	MUSXPG.PRO
403	ERECTNQRK	GQKTNTKS-----	QGTKRKPTECSQ	EDQDPGGGFI	GIELKTLSSKAY	SSD-----	XENXPG.PRO
322	MKECGWPATRTQ	KELALSIRRKVHL	TTTVAQTRIPD	FFAATKSKNFT	PIVEPCE	SLIEDYISANN-----	T CELRAD2.PRO

	500	510	520	530	540	550	560
314	-----	-----	-----	-----	-----	-----	NKTKQKTL MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	KSGKQSTL PFUFEN1.PRO
352	SAKRKEPEPKGST	-----	-----	-----	-----	-----	KKKAKTGAAG HUMFEN1.PRO
350	SAKRKEPEPKGPA	-----	-----	-----	-----	-----	KKKAKTGGAG MUSFEN1.PRO
354	KEQLAAAKRAQE	-----	-----	-----	-----	-----	NKKLNKNKNK YST510.PRO
364	-----	-----	PREYISGDKKLNT	SKRISTATGKL	-----	-----	KK YSTRAD2.PRO
429	RRKKMMASKNSSD	SDSEDNFLASLTP	KTNSSSISIENL	PRKTKLSTSL	-----	-----	KKP SPORAD13.PRO
476	NVQRRTAAKEPKT	SASDSONSVKEAP	VKNGGATTSSSD	SDDDGGKEKML	VTARSVFGKKRR	KLRRARG	HUMXPG.PRO
469	SARQSAAESKIGC	SDVDPDLVRDSP	HGRQGCVSTSSD	SEDGEDKAKTV	LTARPVFGKKRR	KLKSMK-	MUSXPG.PRO
458	-----	GSSSDAEDLP	SGLIDKQSQSGI	VGROKASNK	VESSSSDD	EDRTVMVTAKPV	FQGGKTKSKTMKE XENXPG.PRO
387	WMRKRKRSESP	QILQHHAKRQVP	DRK-----	-----	-----	-----	RSVKIRAFKPYPTDVI CELRAD2.PRO

FIG. 70D

322 DAWFKZ  
335 ESWFKR  
375 KFKRGK  
373 KFRRGK  
377 VTKGRR  
390 ---RKM  
483 SKRRRK  
546 RKRKTZ  
538 RRKKKT  
523 TVKRK  
429 ELGDSD

MJAFEN1.PRO  
PFUFEN1.PRO  
HUMFEN1.PRO  
MUSFEN1.PRO  
YST510.PRO  
YSTRAD2.PRO  
SPORAD13.PRO  
HUMXPG.PRO  
MUSXPG.PRO  
XENXPG.PRO  
CELRAD2.PRO

**FIG. 70E**